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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 :
C12N 15/12, 15/62, C07K 14/705, 16/28, C12N 5/10, C12Q 1/68, G01N 33/68

A1

(11) International Publication Number: WO 95/08627

(43) International Publication Date: 30 March 1995 (30.03.95)

(21) International Application Number: PCT/EP94/02991

(22) International Filing Date: 7 September 1994 (07.09.94)

(30) Priority Data:
93810663.0 20 September 1993 (20.09.93) EP
(34) Countries for which the regional or international application was filed: GB et al.
9416553.7 19 August 1994 (19.08.94) GB

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(81) Designated States: AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, JP, KG, KP, KR, KZ, LK, LR, LT, LV, MD, MG, MN, NO, NZ, PL, RO, RU, SI, SK, TJ, TT, UA, US, UZ, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG), ARIPO patent (KE, MW, SD).

Published
With international search report.

(54) Title: HUMAN METABOTROPIC GLUTAMATE RECEPTOR SUBTYPES (HMR4, HMR6, HMR7) AND RELATED DNA COMPOUNDS

(57) Abstract

The present invention relates to human metabotropic glutamate receptor (hmGluR) proteins, isolated nucleic acids coding therefor, host cells producing the proteins of the invention, methods for the preparation of such proteins, nucleic acids and host cells, and uses thereof. Furthermore, the invention provides antibodies directed against the hmGluR proteins.

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HUMAN METABOTROPIC GLUTAMATE RECEPTOR SUBTYPES (HMR4, HMR6, HMR7) AND RELATED DNA COMPOUNDS.

The present invention relates to human metabotropic glutamate receptor (hmGluR) proteins, isolated nucleic acids coding therefor, host cells producing the proteins of the invention, methods for the preparation of such proteins, nucleic acids and host cells, and uses thereof. Furthermore, the invention provides antibodies directed against the hmGluR proteins of the invention.

Metabotropic glutamate receptors (hmGluR) belong to the class of G-protein (guanine nucleotide binding protein) coupled receptors which upon binding of a glutamatergic ligand may transduce an extracellular signal via an intracellular second messenger system such as calcium ions, a cyclic nucleotide, diacylglycerol and inositol 1,4,5-triphosphate into a physiological response. Possessing seven putative transmembrane spanning segments, preceded by a large extracellular amino-terminal domain and followed by a large carboxy-terminal domain metabotropic glutamate receptors are characterized by a common structure. Based on the degree of sequence identity at the amino acid level the class of mGluR can be divided into different subfamilies comprising individual receptor subtypes (Nakanishi, Science 258, 597-603 (1992)). Each mGluR subtype is encoded by a unique gene. Regarding the homology of an individual mGluR subtype to another subtype of a different subfamily, the amino acid sequences are less than about 50 % identical. Within a subfamily the degree of sequence identity is generally less than about 70 %. Thus a particular subtype may be characterized by its amino acid sequence homology to another mGluR subtype, especially a subtype of the same mammalian species. Furthermore, a particular subtype may be characterized by its region and tissue distribution, its cellular and subcellular expression pattern or by its distinct physiological profile, e.g. by its electrophysiological and pharmacological properties.

The amino acid L-glutamate being the major excitatory neurotransmitter, glutamatergic systems are presumed to play an important role in numerous neuronal processes including fast excitatory synaptic transmission, regulation of neurotransmitter releases, long-term potentation, learning and memory, developmental synaptic plasticity, hypoxic-ischemic damage and neuronal cell death, epileptiform seizures, as well as the pathogenesis of several neurodegenerative disorders. Up to today, no information is available on human metabotropic glutamate receptor (hmGluR) subtypes, e.g. on their amino acid sequence or tissue distribution. This lack of knowledge particularly hampers the search for human therapeutic agents capable of specifically influencing any disorder attributable to a defect in the glutamatergic system. In view of the potential physiological and pathological

significance of metabotropic glutamate receptors, there is a need for human receptor subtypes and cells producing such subtypes in amounts sufficient for elucidating the electrophysiological and pharmacological properties of these proteins. For example, drug screening assays require purified human receptor proteins in an active form, which have not yet been attainable.

It is an object of the present invention to fulfill this need, namely to provide distinct hmGluR subtypes, nucleic acids coding therefor and host cells producing such subtypes. In particular, the present invention discloses the hmGluR subfamily comprising the subtype designated hmGluR4, and the individual proteins of said subfamily. In the following, said subfamily will be referred to as the hmGluR4 subfamily. Contrary to other hmGluR subtypes the members of this subfamily are potently activated by L-2-amino-4-phosphobutyric acid (AP4) and, when expressed e.g. in Chinese hamster ovary (CHO) cells or baby hamster kidney (BHK) cells, negatively coupled to adenylate cyclase via G protein. Using a system comprising a recombinant hmGluR subtype of the invention in screening for hmGluR reactive drugs offers (among others) the possibilities of attaining a greater number of receptors per cell giving greater yield of reagent and a higher signal to noise ratio in assays as well as increased receptor subtype specificity (potentially resulting in greater biological and disease specificity).

More specifically, the present invention relates to a hmGluR subtype characterized in that its amino acid sequence is more than about 65 % identical to the sequence of the hmGluR4 subtype having the amino acid sequence depicted in SEQ ID NO:2.

According to the invention the expression "hmGluR subtype" refers to a purified protein which belongs to the class of G protein-coupled receptors and which upon binding of a glutamatergic ligand transduces an extracellular signal via an intracellular second messenger system. In such case, a subtype of the invention is characterized in that it modifies the level of a cyclic nucleotide (cAMP, cGMP). Alternatively, signal transduction may occur via direct interaction of the G protein coupled to a receptor subtype of the invention with another membrane protein, such as an ion channel or another receptor. A receptor subtype of the invention is believed to be encoded by a distinct gene which does not encode another metabotropic glutamate receptor subtype. A particular subtype of the invention may be characterized by its distinct physiological profile, preferably by its signal transduction and pharmacological properties. Pharmacological properties are e.g. the selectivity for agonists and antagonist responses.

As defined herein, a glutamatergic ligand is e.g. L-glutamate or another compound interacting with, and particularly binding to, a hmGluR subtype in a glutamate like manner, such as ACPD (1S,3R-1-aminocyclopentane-1,3-dicarboxylic acid), an ACPD-like ligand, e.g. QUIS (quisqualate), AP4, and the like. Other ligands, e.g. (R,S)-α-methylcarboxyphenylglycine (MCPG) or α-methyl-L-AP4, may interact with a receptor of the invention in such a way that binding of glutamatergic ligand is prevented.

As used hereinbefore or hereinafter, the terms "purified" or "isolated" are intended to refer to a molecule of the invention in an enriched or pure form obtainable from a natural source or by means of genetic engineering. The purified proteins, DNAs and RNAs of the invention may be useful in ways that the proteins, DNAs and RNAs as they naturally occur are not, such as identification of compounds selectively modulating the expression or the activity of a hmGluR of the invention.

Purified hmGluR of the invention means a member of the hmGluR4 subfamily which has been identified and is free of one or more components of its natural environment. Purified hmGluR includes purified hmGluR of the invention in recombinant cell culture. The enriched form of a subtype of the invention refers to a preparation containing said subtype in a concentration higher than natural, e.g. a cellular membrane fraction comprising said subtype. If said subtype is in a pure form it is substantially free from other macromolecules, particularly from naturally occurring proteinaceous contaminations. If desired, the subtype of the invention may be solubilized. A preferred purified hmGluR subtype of the invention is a recombinant protein. Preferably, the subtype of the invention is in an active state meaning that it has both ligand binding and signal transduction activity. Receptor activity is measured according to methods known in the art, e.g. using a binding assay or a functional assay, e.g. an assay as described below.

Preferred hmGluR subtypes of the hmGluR4 subfamily are subtypes hmGluR4, hmGluR7 and hmGluR6. A particularly preferred hmGluR4 subtype is the protein having the amino acid sequence set forth in SEQ ID NO:2. A hmGluR7-type protein may comprise a polypeptide selected from the group consisting of the polypeptides having the amino acid sequences depicted in SEQ ID NOs: 4, 6, 8 and 10, respectively. Such hmGluR7 subtype is preferred. Particularly preferred are the hmGluR7 subtypes having the amino acid sequences set forth in SEQ ID NOs: 12 and 14, respectively. A preferred hmGluR6-type protein comprises a polypeptide having the amino acid sequence depicted in SEQ ID

NO:16.

The invention is further intended to include variants of the receptor subtypes of the invention. For example, a variant of a hmGluR subtype of the invention is a functional or immunological equivalent of said subtype. A functional equivalent is a protein, particularly a human protein, displaying a physiological profile essentially identical to the profile characteristic of said particular subtype. The physiological profile in vitro and in vivo includes receptor effector function, electrophysiological and pharmacological properties, e.g. selective interaction with agonists or antagonists. Exemplary functional equivalents may be splice variants encoded by mRNA generated by alternative splicing of a primary transcript, amino acid mutants and glycosylation variants. An immunological equivalent of a particular hmGluR subtype is a protein or peptide capable of generating antibodies specific for said subtype. Portions of the extracellular domain of the receptor, e.g. peptides consisting of at least 6 to 8 amino acids, particularly 20 amino acids, are considered particularly useful immunological equivalents.

Further variants included herein are membrane-bound and soluble fragments and covalent or aggregative conjugates with other chemical moieties, these variants displaying one or more receptor functions, such as ligand binding or signal transduction. Exemplary fragments of hmGluR subtypes of the invention are the polypeptides having the amino acid sequences set forth in SEQ ID NOs: 4, 6, 8, 10 and 16, respectively. The fragments of the invention are obtainable from a natural source, by chemical synthesis or by recombinant techniques. Due to their capability of competing with the endogenous counterpart of a hmGluR subtype of the invention for its endogenous ligand, fragments, or derivatives thereof, comprising the ligand binding domain are envisaged as therapeutic agents.

Covalent derivatives include for example aliphatic esters or amides of a receptor carboxyl group, O-acyl derivatives of hydroxyl group containing residues and N-acyl derivatives of amino group containing residues. Such derivatives can be prepared by linkage of functionalities to reactable groups which are found in the side chains and at the N- and C-terminus of the receptor protein. The protein of the invention can also be labeled with a detectable group, for example radiolabeled, covalently bound to rare earth chelates or conjugated to a fluorescent moiety.

Further derivatives are covalent conjugates of a protein of the invention with another

protein or peptide (fusion proteins). Examples are fusion proteins comprising different portions of different glutamate receptors. Such fusion proteins may be useful for changing the coupling to G-proteins and/or improving the sensitivity of a functional assay. For example, in such fusion proteins or chimeric receptors, the intracellular domains of a subtype of the invention may be replaced with the corresponding domains of another mGluR subtype, particularly another hmGluR subtype, e.g. a hmGLuR subtype belonging to another subfamily. Particularly suitable for the construction of such a chimeric receptor are the intracellular domains of a receptor which activates the phospholipase C/Ca^{2+} signaling pathway, e.g. mGluR1 (Masu et al., Nature 349, 760-765) or mGluR5. An intracellular domain suitable for such an exchange is e.g. the second intracellular loop, also referred to as i2 (Pin et al., EMBO J. 13, 342-348 (1994)). Thus it is possible to analyze the interaction of a test compound with a ligand binding domain of a receptor of the invention using an assay for calcium ions. The chimeric receptor according to the invention can be synthesized by recombinant techniques or agents known in the art as being suitable for crosslinking proteins.

Aggregative derivatives are e.g. adsorption complexes with cell membranes.

In another embodiment, the present invention relates to a composition of matter comprising a hmGluR subtype of the invention.

The proteins of the invention are useful e.g. as immunogens, in drug screening assays, as reagents for immunoassays and in purification methods, such as for affinity purification of a binding ligand.

A protein of the invention is obtainable from a natural source, e.g. by isolation from brain tissue, by chemical synthesis or by recombinant techniques.

The invention further provides a method for preparing a hmGluR subtype of the invention characterized in that suitable host cells producing a receptor subtype of the invention are multiplied in vitro or in vivo. Preferably, the host cells are transformed (transfected) with a hybrid vector comprising an expression cassette comprising a promoter and a DNA sequence coding for said subtype which DNA is controlled by said promoter. Subsequently, the hmGluR subtype of the invention may be recovered. Recovery comprises e.g. isolating the subtype of the invention from the host cells or isolating the host cells comprising the subtype, e.g. from the culture broth. Particularly preferred is a

method for preparation of a functionally active receptor.

HmGluR muteins may be produced from a DNA encoding a hmGluR protein of the invention which DNA has been subjected to in vitro mutagenesis resulting e.g. in an addition, exchange and/or deletion of one or more amino acids. For example, substitutional, deletional and insertional variants of a hmGluR subtype of the invention are prepared by recombinant methods and screened for immuno-crossreactivity with the native forms of the hmGluR.

A protein of the invention may also be derivatized in vitro according to conventional methods known in the art.

Suitable host cells include eukaryotic cells, e.g. animal cells, plant cells and fungi, and prokaryotic cells, such as gram-positive and gram-negative bacteria, e.g. E. coli. Preferred eukaryotic host cells are of amphibian or mammalian origin.

As used herein, in vitro means ex vivo, thus including e.g. cell culture and tissue culture conditions.

This invention further covers a nucleic acid (DNA, RNA) comprising a purified, preferably recombinant, nucleic acid (DNA, RNA) coding for a subtype of the invention, or a fragment of such a nucleic acid. In addition to being useful for the production of the above recombinant hmGluR proteins, these nucleic acid are useful as probes, thus readily enabling those skilled in the art to identify and/or isolate nucleic acid encoding a hmGluR protein of the invention. The nucleic acid may be unlabeled or labeled with a detectable moiety. Furthermore, nucleic acid according to the invention is useful e.g. in a method for determining the presence of hmGluR, said method comprising hybridizing the DNA (or RNA) encoding (or complementary to) hmGluR to test sample nucleic acid and to determine the presence of hmGluR.

Purified hmGluR encoding nucleic acid of the invention includes nucleic acid that is free from at least one contaminant nucleic acid with which it is ordinarily associated in the natural source of hmGluR nucleic acid. Purified nucleic acids thus is present in other than in the form or setting in which it is found in nature. However, purified hmGluR nucleic acid embraces hmGluR nucleic acid in ordinarily hmGluR expressing cells where the nucleic acid is in a chromosomal location different from that of natural cells or is

otherwise flanked by a different DNA sequence than that found in nature.

In particular, the invention provides a purified or isolated DNA molecule encoding a hmGluR subtype of the invention, or a fragment of such DNA. By definition, such a DNA comprises a coding single DNA, a double stranded DNA consisting of said coding DNA and complementary DNA thereto, or this complementary (single stranded) DNA itself. Preferred is a DNA coding for the above captioned preferred hmGluR subtypes, or a fragment thereof. Furthermore, the invention relates to a DNA comprising such a DNA.

More specifically, preferred is a DNA coding for a hmGluR4 subtype or a portion thereof, particularly a DNA encoding the hmGluR4 subtype having the amino acid sequence set forth in SEQ ID NO:2, e.g. the DNA with the nucleotide sequence set forth in SEQ ID NO:1. An exemplary DNA fragment coding for a portion of hmGluR4 is the hmGluR4-encoding portion of cDNA cmR20 as described in the Examples.

Equally preferred is a DNA encoding a hmGluR7 subtype, particularly a DNA encoding any of the hmGluR7 subtypes having the amino acid sequences set forth in SEQ ID NOs: 12 and 14, respectively, e.g. the DNAs with the nucleotide sequences set forth in SEQ ID NOs: 11 and 13, respectively. The invention further provides a DNA fragment encoding a portion of a hmGluR7 subtype, particularly the hmGluR7 subtypes identified as preferred above. Exemplary hmGluR7 DNA fragments include the hmGluR7-encoding portions of cDNAs cmR2, cmR3, cmR5 and cR7PCR1, as described in the Examples, or a DNA fragment which encodes substantially the same amino acid sequence as that encoded by the hmGluR7-encoding portion of plasmid cmR2 deposited with the DSM on September 13, 1993, under accession number DSM 8550. These DNAs encode portions of putative splice variants of the hmGluR7 subtype described herein.

Also preferred is a DNA encoding a hmGluR6 subtype or a portion thereof, particularly a DNA encoding the portion of the hmGluR6 subtype, the amino acid sequence of which is depicted in SEQ ID NO:16, or a DNA which encodes substantially the same amino acid sequence as that encoded by the hmGluR6-encoding portion of plasmid cmR1 deposited with the DSM on September 13, 1993, under accession number DSM 8549. An exemplary DNA sequence is set forth in SEQ ID NO:15.

The nucleic acid sequences provided herein may be employed to identify DNAs encoding further hmGluR subtypes. For example, nucleic acid sequences of the invention may be

used for identifying DNAs encoding further hmGluR subtypes belonging to the subfamily comprising hmGluR 4. A method for identifying such DNA comprises contacting human DNA with a nucleic acid probe described above and identifying DNA(s) which hybridize to that probe.

Exemplary nucleic acids of the invention can alternatively be characterized as those nucleic acids which encode a hmGluR subtype of the invention and hybridize to a DNA sequence set forth in SEQ ID NOs. 1, 3, 5, 7, 9, 11, 13 or 15, or a selected portion (fragment) of said DNA sequence. For example, selected fragments useful for hybridization are the protein-encoding portions of said DNAs. Preferred are such DNAs encoding a hmGluR of the invention which hybridize under high-stringency conditions to the above-mentioned DNAs.

Stringency of hybridization refers to conditions under which polynucleic acids hybrids are stable. Such conditions are evident to those of ordinary skill in the field. As known to those of skill in the art, the stability of hybrids is reflected in the melting temperature (T_m) of the hybrid which decreases approximately 1 to 1.5°C with every 1% decrease in sequence homology. In general, the stability of a hybrid is a function of sodium ion concentration and temperature. Typically, the hybridization reaction is performed under conditions of higher stringency, followed by washes of varying stringency.

As used herein, high stringency refers to conditions that permit hybridization of only those nucleic acid sequences that form stable hybrids in 1 M Na^+ at 65-68 °C. High stringency conditions can be provided, for example, by hybridization in an aqueous solution containing 6x SSC, 5x Denhardt's, 1 % SDS (sodium dodecyl sulfate), 0.1 Na^+ pyrophosphate and 0.1 mg/ml denatured salmon sperm DNA as non specific competitor. Following hybridization, high stringency washing may be done in several steps, with a final wash (about 30 min) at the hybridization temperature in 0.2- 0.1x SSC, 0.1 % SDS.

Moderate stringency refers to conditions equivalent to hybridization in the above described solution but at about 60-62 °C. In that case the final wash is performed at the hybridization temperature in 1x SSC, 0.1 % SDS.

Low stringency refers to conditions equivalent to hybridization in the above described solution at about 50-52°C. In that case, the final wash is performed at the hybridization temperature in 2x SSC, 0.1 % SDS.

It is understood that these conditions may be adapted and duplicated using a variety of buffers, e.g. formamide-based buffers, and temperatures. Denhart's solution and SSC are well known to those of skill in the art as are other suitable hybridization buffers (see, e.g. Sambrook, J., Fritsch, E.F. and Maniatis, T. (1989) Molecular Cloning: A Laboratory Manual (2nd edition), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, USA, or Ausubel, F. M., et al. (1993) Current Protocols in Molecular Biology, Greene and Wiley, USA). Optimal hybridization conditions have to be determined empirically, as the length and the GC content of the probe also play a role.

Given the guidance of the present invention, the nucleic acids of the invention are obtainable according to methods well known in the art. The present invention further relates to a process for the preparation of such nucleic acids.

For example, a DNA of the invention is obtainable by chemical synthesis, by recombinant DNA technology or by polymerase chain reaction (PCR). Preparation by recombinant DNA technology may involve screening a suitable cDNA or genomic library. A suitable method for preparing a DNA or of the invention comprises the synthesis of a number of oligonucleotides, their amplification by PCR methods, and their splicing to give the desired DNA sequence. Suitable libraries are commercially available, e.g. the libraries employed in the Examples, or can be prepared from neural or neuronal tissue samples, e.g. hippocampus and cerebellum tissue, cell lines and the like.

For individual hmGluR subtypes (and splice variants) of the invention the expression pattern in neural or neuronal tissue may vary. Thus, in order to isolate cDNA encoding a particular subtype (or splice variant), it is advantageous to screen libraries prepared from different suitable tissues or cells. As a screening probe, there may be employed a DNA or RNA comprising substantially the entire coding region of a hmGluR subtype of the invention, or a suitable oligonucleotide probe based on said DNA. A suitable oligonucleotide probe (for screening involving hybridization) is a single stranded DNA or RNA that has a sequence of nucleotides that includes at least 14 contiguous bases that are the same as (or complementary to) any 14 or more contiguous bases set forth in any of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13 and 15. The probe may be labeled with a suitable chemical moiety for ready detection. The nucleic acid sequences selected as probes should be of sufficient length and sufficiently unambiguous so that false positive results are minimized.

Preferred regions from which to construct probes include 5' and/or 3' coding sequences, sequences predicted to encode ligand binding sites, and the like. For example, either the full-length cDNA clones disclosed herein or fragments thereof can be used as probes. Preferably, nucleic acid probes of the invention are labeled with suitable label means for ready detection upon hybridization. For example, a suitable label means is a radiolabel. The preferred method of labelling a DNA fragment is by incorporating ^{32}P-labelled α-dATP with the Klenow fragment of DNA polymerase in a random priming reaction, as is well known in the art. Oligonucleotides are usually end-labeled with ^{32}P-labeled γ-ATP and polynucleotide kinase. However, other methods (e.g. non-radioactive) may also be used to label the fragment or oligonucleotide, including e.g. enzyme labelling and biotinylation.

After screening the library, e.g. with a portion of DNA including substantially the entire hmGluR-encoding sequence or a suitable oligonucleotide based on a portion of said DNA, positive clones are identified by detecting a hybridization signal; the identified clones are characterized by restriction enzyme mapping and/or DNA sequence analysis, and then examined, e.g. by comparison with the sequences set forth herein, to ascertain whether they include DNA encoding a complete hmGluR (i.e., if they include translation initiation and termination codons). If the selected clones are incomplete, they may be used to rescreen the same or a different library to obtain overlapping clones. If the library is genomic, then the overlapping clones may include exons and introns. If the library is a cDNA library, then the overlapping clones will include an open reading frame. In both instances, complete clones may be identified by comparison with the DNAs and deduced amino acid sequences provided herein.

Furthermore, in order to detect any abnormality of an endogenous hmGluR subtype of the invention genetic screening may be carried out using the nucleotide sequences of the invention as hybridization probes. Also, based on the nucleic acid sequences provided herein antisense-type therapeutic agents may be designed.

It is envisaged that the nucleic acid of the invention can be readily modified by nucleotide substitution, nucleotide deletion, nucleotide insertion or inversion of a nucleotide stretch, and any combination thereof. Such modified sequences can be used to produce a mutant hmGluR subtype which differs from the receptor subtypes found in nature. Mutagenesis may be predetermined (site-specific) or random. A mutation which is not a silent mutation

must not place sequences out of reading frames and preferably will not create complementary regions that could hybridize to produce secondary mRNA structures such as loops or hairpins.

The cDNA or genomic DNA encoding native or mutant hmGluR of the invention can be incorporated into vectors for further manipulation. Furthermore, the invention concerns a recombinant DNA which is a hybrid vector comprising at least one of the above mentioned DNAs.

The hybrid vectors of the invention comprise an origin of replication or an autonomously replicating sequence, one or more dominant marker sequences and, optionally, expression control sequences, signal sequences and additional restriction sites.

Preferably, the hybrid vector of the invention comprises an above described nucleic acid insert operably linked to an expression control sequence, in particular those described hereinafter.

Vectors typically perform two functions in collaboration with compatible host cells. One function is to facilitate the cloning of the nucleic acid that encodes the hmGluR subtype of the invention, i.e. to produce usable quantities of the nucleic acid (cloning vectors). The other function is to provide for replication and expression of the gene constructs in a suitable host, either by maintenance as an extrachromosomal element or by integration into the host chromosome (expression vectors). A cloning vector comprises the DNAs as described above, an origin of replication or an autonomously replicating sequence, selectable marker sequences, and optionally, signal sequences and additional restriction sites. An expression vector additionally comprises expression control sequences essential for the transcription and translation of the DNA of the invention. Thus an expression vector refers to a recombinant DNA construct, such as a plasmid, a phage, recombinant virus or other vector that, upon introduction into a suitable host cell, results in expression of the cloned DNA. Suitable expression vectors are well known in the art and include those that are replicable in eukaryotic and/or prokaryotic cells.

Most expression vectors are capable of replication in at least one class of organisms but can be transfected into another organism for expression. For example, a vector is cloned in E. coli and then the same vector is transfected into yeast or mammalian cells even though it is not capable of replicating independently of the host cell chromosome. DNA may also

be amplified by insertion into the host genome. However, the recovery of genomic DNA encoding hmGluR is more complex than that of exogenously replicated vector because restriction enzyme digestion is required to excise hmGluR DNA. DNA can be amplified by PCR and be directly transfected into the host cells without any replication component.

Advantageously, expression and cloning vector contain a selection gene also referred to as selectable marker. This gene encodes a protein necessary for the survival or growth of transformed host cells grown in a selective culture medium. Host cells not transformed with the vector containing the selection gene will not survive in the culture medium. Typical selection genes encode proteins that confer resistance to antibiotics and other toxins, e.g. ampicillin, neomycin, methotrexate or tetracycline, complement auxotrophic deficiencies, or supply critical nutrients not available from complex media.

Since the amplification of the vectors is conveniently done in E. coli, an E. coli genetic marker and an E. coli origin of replication are advantageously included. These can be obtained from E. coli plasmids, such as pBR322, Bluescript vector or a pUC plasmid.

Suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up hmGluR nucleic acid, such as dihydrofolate reductase (DHFR, methotrexate resistance), thymidine kinase, or genes confering resistance to G418 or hygromycin. The mammalian cell transfectants are placed under selection pressure which only those transfectants are uniquely adapted to survive which have taken up and are expressing the marker.

Expression and cloning vectors usually contain a promoter that is recognized by the host organism and is operably linked to hmGluR nucleic acid. Such promoter may be inducible or constitutive. The promoters are operably linked to DNA encoding hmGluR by removing the promoter from the source DNA by restriction enzyme digestion and inserting the isolated promoter sequence into the vector. Both the native hmGluR promoter sequence and many heterologous promoters may be used to direct amplification and/or expression of hmGluR DNA. However, heterologous promoters are preferred, because they generally allow for greater transcription and higher yields of expressed hmGluR as compared to native hmGluR promoter.

Promoters suitable for use with prokaryotic hosts include, for example, the β-lactamase and lactose promoter systems, alkaline phosphatase, a tryptophan (trp) promoter system

and hybrid promoters such as the tac promoter. Their nucleotide sequences have been published, thereby enabling the skilled worker operably to ligate them to DNA encoding hmGluR, using linkers or adaptors to supply any required restriction sites. Promoters for use in bacterial systems will also generally contain a Shine-Delgarno sequence operably linked to the DNA encoding hmGluR.

HmGluR gene transcription from vectors in mammalian host cells may be controlled by promoters compatible with the host cell systems, e.g. promoters derived from the genomes of viruses. Suitable plasmids for expression of a hmGluR subtype of the invention in eukaryotic host cells, particularly mammalian cells, are e.g. cytomegalovirus (CMV) promoter-containing vectors, RSV promoter-containing vectors and SV40 promoter-containing vectors and MMTV LTR promoter-containing vectors. Depending on the nature of their regulation, promoters may be constitutive or regulatable by experimental conditions.

Transcription of a DNA encoding a hmGluR subtype according to the invention by higher eukaryotes may be increased by inserting an enhancer sequence into the vector.

The various DNA segments of the vector DNA are operatively linked, i.e. they are contiguous and placed into a functional relationship to each other.

Construction of vectors according to the invention employs conventional ligation techniques. Isolated plasmids or DNA fragments are cleaved, tailored, and religated in the form desired to generate the plasmids required. If desired, analysis to confirm correct sequences in the constructed plasmids is performed in a manner known in the art. Suitable methods for constructing expression vectors, preparing in vitro transcripts, introducing DNA into host cells, and performing analyses for assessing hmGluR expression and function are known to those skilled in the art. Gene presence, amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, northern blotting to quantitate the transcription of mRNA, dot blotting (DNA or RNA analysis), in situ hybridization, using an appropriately labelled probe based on a sequence provided herein, binding assays, immunodetection and functional assays. Suitable methods include those decribed in detail in the Examples. Those skilled in the art will readily envisage how these methods may be modified, if desired.

The invention further provides host cells capable of producing a hmGluR subtype of the

invention and including heterologous (foreign) DNA encoding said subtype.

The nucleic acids of the invention can be expressed in a wide variety of host cells, e.g. those mentioned above, that are transformed or transfected with an appropriate expression vector. The receptor of the invention (or a portion thereof) may also be expressed as a fusion protein. Recombinant cells can then be cultured under conditions whereby the protein (s) encoded by the DNA of the invention is (are) expressed.

Suitable prokaryotes include eubacteria, such as Gram-negative or Gram-prositive organisms, such as E. coli, e.g. E. coli K-12 strains, DH5α and HB 101, or Bacilli. Further host cells suitable for hmGluR encoding vectors include eukaryotic microbes such as filamentous fungi or yeast, e.g. Saccharomyces cerevisiae. Higher eukaryotic cells include insect, amphebian and vertebrate cells, particularly mammalian cells, e.g. neuroblastoma cell lines or fibroblast derived cell lines. Examples of preferred mammalian cell lines are e.g. HEK 293 cells, CHO cells, CV1 cells, BHK cells, L cells, LLCPK-1 cells, GH3 cells, L cells and COS cells. In recent years propagation of vertebrate cells in culture (tissue culture) has become a routine procedure. The host cells referred to in this application comprise cells in in vitro culture as well as cells that are within a host animal.

Suitable host cells for expression of an active recombinant hmGluR of the invention advantageously express endogenous or recombinant G-proteins. Preferred are cells producing little, if any, endogenous metabotropic glutamate receptor. DNA may be stably incorporated into the cells or may be transiently expressed according to conventional methods.

Stably transfected mammalian cells may be prepared by transfecting cells with an expression vector having a selectable marker gene, and growing the transfected cells under conditions selective for cells expressing the marker gene. To prepare transient transfectants, mammalian cells are transfected with a reporter gene to monitor transfection efficiency.

To produce such stably or transiently transfected cells, the cells should be transfected with a sufficient amount of hmGluR-encoding nucleic acid to form hmGluR of the invention. The precise amounts of DNA encoding hmGluR of the invention may be empirically determined and optimized for a particular cell and assay.

A DNA of the invention may also be expressed in non-human transgenic animals, particularly transgenic warm-blooded animals. Methods for producing transgenic animals, including mice, rats, rabbits, sheep and pigs, are known in the art and are disclosed, for example by Hammer et al. (Nature 315, 680-683, 1985). An expression unit including a DNA of the invention coding for a hmGluR together with appropriately positioned expression control sequences, is introduced into pronuclei of fertilized eggs. Introduction may be achieved, e.g. by microinjection. Integration of the injected DNA is detected, e.g. by blot analysis of DNA from suitable tissue samples. It is preferred that the introduced DNA be incorporated into the germ line of the animal so that it is passed to the animal's progeny. Preferably, a transgenic animal is developped by targeting a mutation to disrupt a hmGluR sequence. Such an animal is useful e.g. for studying the role of a metabotropic receptor in metabolism .

Furthermore, a knock-out animal may be developed by introducing a mutation in the hmGluR sequence, thereby generating an animal which does not express the functional hmGluR gene anymore. Such knock-out animal is useful e.g. for studying the role of metabotropic receptor in metabolism. methods for producing knock-out mice are known in the art.

Host cells are transfected or transformed with the above-captioned expression or cloning vectors of this invention and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. Heterologous DNA may be introduced into host cells by any method known in the art, such as transfection with a vector encoding a heterologous DNA by the calcium phosphate coprecipitation technique, by electroporation or by lipofectin-mediated. Numerous methods of transfection are known to the skilled worker in the field. Successful transfection is generally recognized when any indication of the operation of this vector occurs in the host cell. Transformation is achieved using standard techniques appropriate to the particular host cells used.

Incorporation of cloned DNA into a suitable expression vector, transfection of eukaryotic cells with a plasmid vector or a combination of plasmid vectors, each encoding one or more distinct genes or with linear DNA, and selection of transfected cells are well known in the art (see, e.g. Sambrook et al. (1989) Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor Laboratory Press).

Transfected or transformed cells are cultured using media and culturing methods known in the art, preferably under conditions, whereby hmGluR encoded by the DNA is expressed. The composition of suitable media is known to those in the art, so that they can be readily prepared. Suitable culturing media are also commercially available.

While the DNA provided herein may be expressed in any suitable host cell, e.g. those referred to above, preferred for expression of DNA encoding functional hmGluR are eukaryotic expression systems, particularly mammalian expression systems, including commercially available systems and other systems known to those of skill in the art.

Human mGluR DNA of the invention is ligated into a vector, and introduced into suitable host cells to produce transformed cell lines that express a particular hmGluR subtype of the invention, or specific combinations of subtypes. The resulting cell line can then be produced in amounts sufficient for reproducible qualitative and quantitative analysis of the effects of a receptor agonist, antagonist or allosteric modulator. Additionally, mRNA may be produced by in vitro transcription of a DNA encoding a subtype of the invention. This mRNA may be injected into Xenopus oocytes where the mRNA directs the synthesis of the active receptor subtype. Alternatively, the subtype-encoding DNA can be directly injected into oocytes. The transfected mammalian cells or injected oocytes may then be employed in an drug screening assay provided hereinafter. Such drugs are useful in diseases associated with pathogenesis of a hmGluR subtype of the invention. Such diseases include diseases resulting from excessive action of glutamate preferentially mediated by hmGluRs, such as stroke, epilepsy and chronic neurogenerative diseases. Particularly useful for assessing the specific interaction of compounds with specific hmGluR subtypes are stably transfected cell lines expressing a hmGluR of the invention.

Thus host cells expressing hmGluR of the invention are useful for drug screening and it is a further object of the present invention to provide a method for identifying a compound or signal which modulates the activity of hmGluR, said method comprising exposing cells containing heterologous DNA encoding hmGluR of the invention, wherein said cells produce functional hmGluR, to at least one compound or signal whose ability to modulate the activity of said hmGluR is sought to be determined, and thereafter monitoring said cells for changes caused by said modulation. Such an assay enables the identification of agonists, antagonists and allosteric modulators of a hmGluR of the invention.

In a further aspect, the invention relates to an assay for identifying compounds which modulate the activity of a hmGluR subtype of the invention, said assay comprising:
- contacting cells expressing an active hmGluR subtype of the invention and containing heterologous DNA encoding said hmGluR subtype with at least one compound to be tested for its ability to modulate the activity of said receptor, and
- analysing cells for a difference in second messenger level or receptor activity.

In particular, the invention covers an assay for identifying compounds which modulate the activity of a hmGluR subtype of the invention, said assay comprising:
- contacting cells expressing active hmGluR of the invention and containing heterologous DNA encoding said hmGluR subtype with at least one compound to be tested for its ability to modulate the activity of said receptor, and
- monitoring said cells for a resulting change in second messenger activity.
The result obtained in the assay is compared to an assay suitable as a negative control.

Assay methods generally require comparison to various controls. A change in receptor activity or in second messenger level is said to be induced by a test compound if such an effect does not occur in the absence of the test compound. An effect of a test compound on a receptor subtype of the invention is said to be mediated by said receptor if this effect is not observed in cells not expressing the receptor.

As used herein, a compound or signal that modulates the activity of a hmGluR of the invention refers to a compound or signal that alters the response pathway mediated by said hmGluR within a cell (as compared to the absence of said hmGluR). A response pathway is activated by an extracellular stimulus, resulting in a change in second messenger concentration or enzyme activity, or resulting in a change of the activity of a membrane-bound protein, such as a receptor or ion channel. A variety of response pathways may be utilized, including for example, the adenylate cyclase response pathway, the phospholipase C/intracellular calcium ion response pathway or coupling to an ion channel. Assays to determine adenylate cyclase activity are well known in the art, and include e.g. the assay disclosed by Nakajima et al., J. Biol. Chem. 267, 2437-2442 (1992))

Thus cells expressing hmGluR of the invention may be employed for the identification of compounds, particularly low molecular weight molecules capable of acting as glutamate agonists or antagonists. Preferred are low molecular weight molecules of less than 1,000 Dalton. Within the context of the present invention, an agonist is understood to refer to a

molecule that is capable of interacting with a receptor, thus mimicking the action of L-glutamate. In particular, a glutamate agonist is characterized by its ability to interact with a hmGluR of the invention, and thereby increasing or decreasing the stimulation of a response pathway within a cell. For example, an agonist increases or decreases a measurable parameter within the host cell, such as the concentration of a second messenger, as does the natural ligand increase or decrease said parameter. For example, in a suitable test system, wherein hmGluR of the invention is negatively coupled to adenylate cyclase, e.g. CHO or BHK cells expressing a hmGluR of the invention, such an agonist is capable of modulating the function of said hmGluR such that the intracellular concentration of cAMP is decreased.

By contrast, in situations where it is desirable to tone down the activity of hmGluR, antagonizing molecules are useful. Within the context of the present invention, an antagonist is understood to refer to a molecule that is capable of interacting with a receptor or with L-glutamate, but which does not stimulate a response pathway within a cell. In particular, glutamate antagonists are generally identified by their ability to interact with a hmGluR of the invention, and thereby reduce the ability of the natural ligand to stimule a response pathway within a cell, e.g. by interfering with the binding of L-glutamate to a hmGluR of the invention or by inhibiting other cellular functions required for the activity of hmGluR. For example, in a suitable assay, e.g. an assay involving CHO or BHK cells expressing a hmGluR subtype of the invention, a glutamate antagonist is capable of modulating the activity of a hmGluR of the invention such that the ability of the natural ligand to decrease the intracellular cAMP concentration is weakened. Yet another alternative to achieve an antagonistic effect is to rely on overexpression of antisense hmGluR RNA. Preferred is an agonist or antagonist selectively acting on a receptor of the hmGluR4 subfamily, e.g. hmGluR4, hmGluR6 or hmGluR7. Particularly useful is an agonist or antagonist specifically modulating the activity of a particular hmGluR subtype without affecting the activity of any other subtype.

An allosteric modulator of a hmGluR of the invention interacts with the receptor protein at another site than L-glutamate, thus acting as agonist or antagonist. Therefore, the screening assays decribed herein are also useful for detecting an allosteric modulator of a receptor of the invention. For example, an allosteric modulator acting as agonist may enhance the specific interaction between a hmGluR of the invention and L-glutamate. If an allosteric modulator acts as an antagonist, it may e.g. interact with the receptor protein in such a way that binding of the agonist is functionally less effective.

An in vitro assay for a glutamate agonist or antagonist may require that a hmGluR of the invention is produced in sufficient amounts in a functional form using recombinant DNA methods. An assay is then designed to measure a functional property of the hmGluR protein, e.g. interaction with a glutamatergic ligand. Production of a hmGluR of the invention is regarded as occurring in sufficient amounts, if activity of said receptor results in a measurable response.

For example, mammalian cells, e.g. HEK293 cells, L cells, CHO-K1 cells, LLCPK-1 cells or GH3 cells (available e.g. from the American Tissue Type Culture Collection) are adapted to grow in a glutamate reduced, preferably a glutamate free, medium. A hmGluR expression plasmid, e.g. a plasmid described in the Examples, is transiently transfected into the cells, e.g. by calcium-phosphate precipitation (Ausubel, F. M., et al. (1993) Current Protocols in Molecular Biology, Greene and Wiley, USA). Cell lines stably expressing a hmGluR of the invention may be generated e.g. by lipofectin-mediated transfection with hmGluR expression plasmids and a plasmid comprising a selectable marker gene, e.g. pSV2-Neo (Southern and Berg, J. Mol. Appl. Genet. 1, 327-341 (1982)), a plasmid vector encoding the G-418 resistence gene. Cells surviving the selection are isolated and grown in the selection medium. Resistant clonal cell lines are analyzed, e.g. for immunoreactivity with subtype-specific hmGluR antibodies or by assays for hmGluR functional responses following agonist addition. Cells producing the desired hmGluR subtype are used in a method for detecting compounds binding to a hmGluR of the invention or in a method for identifying a glutamate agonist or antagonist.

In a further embodiment, the invention provides a method for identifying compounds binding to a hmGluR subtype, said method comprising employing a hmGluR subtype of the invention in a competitive binding assay. The principle underlying a competitive binding assay is generally kown in the art. Briefly, binding assays according to the invention are performed by allowing the compound to be tested for its hmGluR binding capability to compete with a known, suitably labeled, glutamatergic ligand for the binding site at the hmGluR target molecule. A suitably labeled ligand is e.g. a radioactively labeled ligand, such as [^{3}H]glutamate, or a ligand which can be detected by its optical properties, such as absorbance or fluorescence. After removing unbound ligand and test compound the amount of labeled ligand bound to hmGluR is measured. If the amount of labeled ligand is reduced in the presence of the test compound this compound is said to be bound to the target molecule. A competitive binding assay may be performed e.g. with

transformed or transfected host cells expressing a hmGluR of the invention or a membraneous cellular fraction comprising a hmGluR of the invention.

Compound bound to the target hmGluR may modulate the functional properties of hmGluR and may thereby be identified as a glutamate agonist or antagonist in a functional assay.

Functional assays are used to detect a change in the functional activity of a hmGluR of the invention, i.e. to detect a functional response, e.g. as a result of the interaction of the compound to be tested with said hmGluR. A functional response is e.g. a change (difference) in the concentration of a relevant second messenger, or a change in the activity of another membrane-bound protein influenced by the receptor of the invention within cells expressing a functional hmGluR of the invention (as compared to a negative control). Those of skill in the art can readily identify an assay suitable for detecting a change in the level of an intracellular second messenger indicative of the expression of an active hmGluR (functional assay). Examples include cAMP assays (see, e.g. Nakajima et al., J. Biol. Chem. 267, 2437-2442 (1992), cGMP assays (see, e.g. Steiner et al., J. Biol. Chem. 247, 1106-1113 (1972)), phosphatidyl inositol (PI) turnover assays (Nakajima et al., J. Biol. Chem. 267, 2437-2442 (1992)), calcium ion flux assays (Ito et al., J. Neurochem. 56, 531-540 (1991)), arachidonic acid release assays (see, e.g. Felder et al., J. Biol. Chem. 264, 20356-20362 (1989)), and the like.

More specifically, according to the invention a method for detecting a glutamate agonist comprises the steps of (a) exposing a compound to a hmGluR subtype of the invention coupled to a response pathway, under conditions and for a time sufficient to allow interaction of the compound with the receptor and an associated response through the pathway, and (b) detecting an increase or decrease in the stimulation of the response pathway resulting from the interaction of the compound with the hmGluR subtype, relative to the absence of the tested compound and therefrom determining the presence of a glutamate agonist.

A method for identifying a glutamate antagonist comprises the steps of (a) exposing a compound in the presence of a known glutamate agonist to a hmGluR subtype of the invention coupled to a response pathway, under conditions and for a time sufficient to allow interaction of the agonist with the receptor and an associated response through the pathway, and (b) detecting an inhibition of the stimulation of the response pathway by the

agonist resulting from the interaction of the compound with the hmGluR subtype, relative to the stimulation of the response pathway by the glutamate agonist alone and therefrom determining the presence of a glutamate antagonist. Inhibition may be detected, e.g. if the test compound competes with the glutamate agonist for the hmGluR of the invention. Compounds which may be screened utilizing such method are e.g. blocking antibodies specifically binding to the hmGluR subtype. Furthermore, such an assay is useful for the screening for compounds interacting with L-glutamate, e.g. soluble hmGluR fragments comprising part or all of the ligand binding domain.

Preferentially, interaction of an agonist or antagonist with a hmGluR of the invention denotes binding of the agonist or antagonist to said hmGluR.

As employed herein, conditions and times sufficient for interaction of a glutamate agonist or antagonist candidate to the receptor will vary with the source of the receptor, however, conditions generally suitable for binding occur between about 4°C and about 40°C, preferably between about 4°C and about 37°C, in a buffer solution between 0 and 2 M NaCl, preferably between 0 and 0.9 M NaCl, with 0.1 M NaCl being particularly preferred, and within a pH range of between 5 and 9, preferably between 6.5 and 8. Sufficient time for the binding and response will generally be between about 1 ms and about 24 h after exposure.

Within one embodiment of the present invention, the response pathway is a membrane-bound adenylate cyclase pathway, and, for an agonist, the step of detecting comprises measuring a reduction or increase, preferably a reduction, in cAMP production by the membrane-bound adenylate cyclase response pathway, relative to the cAMP production in the relevant control setup. For the purpose of the present invention, it is preferred that the reduction or increase in cAMP production be equivalent or greater than the reduction or increase induced by L-glutamate applied at a concentration corresponding to its IC_{50} concentration. For an antagonist, the step of detecting comprises measuring in the presence of the antagonist a smaller L-glutamate induced decrease or increase in cAMP production by the membrane-bound adenylate cyclase response pathway, as compared to the cAMP production in the absence of the antagonist. The measurement of cAMP may be performed after cell destruction or by a cAMP sensitive molecular probe loaded into the cell, such as a fluorescent dye, which changes its properties, e.g. its fluorescent properties, upon binding of cAMP.

Cyclic AMP production may be measured using methods well known in the art, including for instance, methods described by Nakajima et al., supra, or using commercially available kits, e.g. kits comprising radiolabeled cAMP, e.g. [^{125}I]cAMP or [^{3}H]cAMP. Exemplary kits are the Scintillation Proximity Assay Kit by Amersham, which measures the production of cAMP by competition of iodinated-cAMP with cAMP antibodies, or the Cyclic AMP [^{3}H] Assay Kit by Amersham.

In assay systems using cells expressing receptor subtypes that are negatively coupled to the adenylate cyclase pathway, i.e. which cause a decrease in cAMP upon stimulation and an increase in cAMP upon reduction of stimulation, it is preferred to expose the cells to a compound which reversibly or irreversibly stimulates the adenylate cyclase, e.g. forskolin, or which is a phosphodiesterase inhibitor, such as isobutylmethylxanthine (IBMX), prior to addition of the (potential) receptor agonist or antagonist.

Within another embodiment of the invention, the response pathway is the PI hydrolysis/ Ca^{2+} mobilization pathway. Such an assay for determining the specific interaction of a test compound with a hmGluR subtype of the invention may be functionally linked to changes in the intracellular calcium ion (Ca^{2+}) concentration. Several methods for determining a change in the intracellular concentration of Ca^{2+} are known in the art, e.g. a method involving a calcium ion sensitive fluoroscent dye, such as fura-2 (see Grynkiewisz et al., J. Biol. Chem. 260, 3440-3450, 1985), fluo-3 or Indo-1, such as the calcium fluor QuinZ method describe by Charest et al. (J. Biol. Chem. 259, 8679-8773 (1993)), or the aequorin photoprotein method described by Nakajima-Shimada (Proc. Natl Acad. Sci. USA 88, 6878-6882 (1991)). In one embodiment of the invention, intracellular calcium ion concentration is measured by microfluoremetry in recombinant cells loaded with calcium sensitive fluorescent dyes fluo-3 or fura-2. These measurements may be performed using cells grown in a coverslip allowing the use of an inverted microscope and video-imaging technologies or a fluorescence photometer to measure calcium concentrations at the single cell level. For both approaches, cells transformed with a hmGluR expressing plasmid have to be loaded with the calcium indicator. To this end, the growth medium is removed from the cells and replaced with a solution containing fura-2 or fluo-3. The cells are used for calcium measurements preferentially during the following 8h. The microfluorometry follows standard procedures.

Ca^{2+} signals resulting from functional interaction of compounds with the target molecule can be transient if the compound is applied for a limited time period, e.g. via a perfusion

system. Using transient application several measurements can be made with the same cells allowing for internal controls and high numbers of compounds tested.

Functional coupling of a hmGluR of the invention to Ca^{2+} signaling may be achieved, e.g. in CHO cells, by various methods:
(i) coexpression of a recombinant hmGluR of the invention and a recombinant voltage-gated cation channel, activity of which is functionally linked to the activity of the hmGluR;
(ii) expression of a chimeric hmGluR receptor, which directly stimulates the PI/Ca^{2+} pathway;
(iii) coexpression of a recombinant hmGluR of the invention with a recombinant Ca^{2+}-permeable cAMP dependent cation channel.

In other expression systems functional coupling of a hmGluR to Ca^{2+} signalling may be achieved by transfection of a hmGluR of the invention if these cells naturally express (i) voltage gated Ca channels, activity of which is functionally linked to activity of mGluRs or (ii) Ca^{2+}-permeable cAMP dependent ion channels. For example, GH3 cells which naturally express voltage-gated Ca channels, directly allow application of Ca^{2+} assays to test for hmGluR functional activity by cotransfection of hmGluRs.

Further cell-based screening assays can be designed e.g. by constructing cell lines in which the expression of a reporter protein, i.e. an easily assayable protein, such as β-galactosidase, chloramphenicol acetyltransferase (CAT) or luciferase, is dependent on the function of a hmGluR of the invention. For example, a DNA construct comprising a cAMP response element is operably linked to a DNA encoding luciferase. The resulting DNA construct comprising the enzyme DNA is stably transfected into a host cell. The host cell is then transfected with a second DNA construct containing a first DNA segment encoding a hmGluR of the invention operably linked to additional DNA segments necessary for the expression of the receptor. For example, if binding of a test compound to the hmGluR of the invention results in elevated cAMP levels, the expression of luciferase is induced or decreased, depending on the promoter chosen. The luciferase is exposed to luciferin, and the photons emitted during oxidation of luciferin by the luciferase is measured.

The drug screening assays provided herein will enable identification and design of receptor subtype-specific compounds, particularly ligands binding to the receptor protein,

eventually leading to the development of a disease-specific drug. If designed for a very specific interaction with only one particular hmGluR subtype (or a predetermined selection of hmGluR subtypes) such a drug is most likely to exhibit fewer unwanted side effects than a drug identified by screening with cells that express a(n) (unknown) variety of receptor subtypes. Also, testing of a single receptor subtype of the invention or specific combinations of different receptor subtypes with a variety of potential agonists or antagonists provides additional information with respect to the function and activity of the individual subtypes and should lead to the identification and design of compounds that are capable of very specific interaction with one or more receptor subtypes.

In another embodiment the invention provides polyclonal and monoclonal antibodies generated against a hmGluR subtype of the invention. Such antibodies may useful e.g. for immunoassays including immunohistochemistry as well as diagnostic and therapeutic applications. For example, antibodies specific for the extracellular domain, or portions thereof, of a particular hmGluR subtype can be applied for blocking the endogenous hmGluR subtype.

The antibodies of the invention can be prepared according to methods well known in the art using as antigen a hmGluR subtype of the invention, a fragment thereof or a cell expressing said subtype or fragment. The antigen may represent the active or inactive form of the receptor of the invention. Antibodies may be capable of distinguishing between the active or inactive form. Factors to consider in selecting subtype fragments as antigens (either as synthetic peptide or as fusion protein) include antigenicity, accessibility (i.e. extracellular and cytoplasmic domains) and uniqueness to the particular subtype.

Particularly useful are antibodies selectively recognizing and binding to receptor subtypes of the above described subfamily without binding to a subtype of another subfamily and antibodies selectively recognizing and binding to one particular subtype without binding to any other subtype.
The antibodies of the invention can be administered to a subject in need thereof employing standard methods. One of skill in the art can readily determine dose forms, treatment regimens etc, depending on the mode of administration employed.

The invention particularly relates to the specific embodiments as described in the Examples which serve to illustrate the present invention but should not be construed as a limitation thereof.

Abbreviations: hmGluR = human metabotropic glutamate receptor, nt=nucleotide

Example 1: cDNA encoding hmGluR4

Human mGluR4 cDNA clones are isolated from human fetal brain and human cerebellum cDNA libraries by low stringency hybridization using a radiolabeled rat mGluR4 probe generated by PCR from rat brain cDNA.

1.1 Preparation of poly(A)$^+$ RNA from rat forebrain

Adult male Sprague-Dawley rats are killed by suffocation, their forebrain is removed and immediately frozen in liquid N_2. Total RNA is isolated using the guanidinium thiocyanate-procedure (Chomczynski and Sacchi (1987), Anal. Biochem. 162, 156-159). Enrichment of poly(A)$^+$ RNA is achieved by affinity chromatography on oligo(dT)-cellulose according to standard procedures (Sambrook, J., Fritsch, E.F. and Maniatis, T. (1989) Molecular Cloning: A Laboratory Manual (2nd edition), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, USA).

1.2 First strand cDNA synthesis for PCR

Poly(A)$^+$RNA (mRNA) is reverse-transcribed into DNA by Moloney Murine Leukemia Virus Reverse Transcriptase (M-MLV RT, BRL). 50 µl reactions are set up as follows: 10 µg of rat forebrain poly(A)$^+$RNA in 10 µl sterile H_2O are heated to 70° C for 10 min and then quickly chilled on ice. Then, 10 µl 5x reaction buffer (250 mM Tris-HCl pH 8.3, 375 mM KCl, 15 mM $MgCl_2$), 5 µl 0.1M dithiothreitol, 5 µl mixed dNTP (10mM each of dATP, dCTP, dGTP, dTTP, Pharmacia), 1.25 µl oligo-dT_{12-18} (2mg/ml, Pharmacia), 2.5 µl RNAsin (40U/µl, Promega), 12.25 µl sterile H_2O and 4 µl (200 U/µl) M-MLV RT are added. The reaction is carried out at 37°C for 60 min.

1.3 PCR conditions for generating the rat mGluR4 fragment

The oligodeoxynucleotide primers used for PCR are synthesized by the phosphoramidite method. Sequences are listed in Table 1.

Table 1

P1: 5'- GTCAAGGCCTCGGGCCGGGA -3'

corresponding to bp 1921-1940 of rat mGluR4 cDNA

(Tanabe, et al., (1992), Neuron 8, 169-179)

P2: 5'- CTAGATGGCATGGTTGGTGTA-3'
corresponding to bp 2788-2808 of rat mGluR4 cDNA
(Tanabe, et al., (1992), Neuron 8, 169-179)

Standard PCR-conditions for a 100 µl reaction mixture are: 30 ng of rat forebrain cDNA, 50 pmol each of primers P1 and P2, 200 µmol each of the four deoxynucleoside triphosphates dATP, dCTP, dGTP and dTTP, 10% DMSO in PCR-buffer (10 mM Tris-HCl, pH 8.3, 1.5 mM $MgCl_2$, 50 mM KCl, 10 mM β-mercaptoethanol, 0.05% Tween (w/v), 0.05% NP-40 (w/v)), and 0.5 U AmpliTaq Polymerase (Perkin Elmer Cetus). The amplification is performed using the following conditions: 30 sec denaturing at 93° C, 1 min 30 sec annealing at 56°C, and 3 min extension at 72°C, for a total of 40 cycles. Initial denaturation is carried out for 4 min at 94°C.

1.4 Subcloning of the rat mGluR4 PCR fragment
Restriction endonuclease digestions, use of modifying enzymes, vector preparation (dephosphorylation, gel purification), ligations, transformation of E. coli, and plasmid DNA preparations are performed according to standard procedures (Sambrook, et al. (1989), supra).
The PCR fragment (888 bp) obtained according to the procedure described in 1.3 is ligated into the SmaI site of the Bluescript SK^+ plasmid (Stratagene, La Jolla, USA). The fragment inserted into the Bluescript vector is sequenced from both ends using T7 and T3 primers (Stratagene, La Jolla, USA).

1.5 Preparation of a radiolabeled probe
20-50 ng of the PCR generated rat mGluR4 fragment are gel purified and ^{32}P-labeled by random priming using a DNA Labeling Kit (Boehringer Mannheim).

1.6 cDNA library screening
About $1x10^6$ phages from a human fetal brain library (λZAPII, Stratagene, La Jolla, USA), human hippocampus (λZAP, Stratagene, La Jolla, USA), and a human cerebellum cDNA library (λZAP, Stratagene) are screened for hybridization to the rat mGluR4 fragment. Hybridization is performed in 5x SSC, 0.02% (w/v) Ficoll (Type 400), 0.02% (w/v) Polyvinylpyrrolidone, 0.1% (w/v) SDS, 50 µg/ml Herring Testis DNA. Prehybridization is carried out between 30 min to 3 hours at 58°C. Hybridization is carried out at low stringency at 58°C overnight in the same solution containing the ^{32}P-labeled fragment at a concentration of 1-3x 10^5 cpm/ml. Washes are done three times for 20 min

each at 58°C in 2x SSC/0.1% SDS.
Phages hybridizing to the rat mGluR4 probe are purified by a second and third round of screening under the conditions described above. The cDNA inserts harbored by the purified phages are rescued by in vivo excision using the ExAssist/SOLR system (Stratagene, La Jolla, USA).

1.7 Characterization of isolated cDNA clones
Several cDNA inserts are characterized by restriction enzyme mapping and DNA sequence analysis. One of these clones, cDNA cmR20 (isolated from human cerebellar library) contains an insert of approximately 3.3 kb. Sequence analysis of cmR20 indicates that it contains almost the complete coding region of human mGluR4 including a translation termination codon (nt 158 to 2739, cf. SEQ ID NO:1) as well as approximately 750 nt of 3' untranslated region. The 5' end including the translational start codon is lacking.

1.8 Isolation of the 5' end of human mGluR4
To complete the coding region of human mGluR4 PCR reactions are carried out using human genomic DNA or first strand cDNA of human brain RNA as a template. The sense primer P3 corresponds to the 5' end of the rat mGluR4 cDNA, the antisense primer P4 to nt 440-459 of the rat mGluR4 cDNA.

Table 2

P3: 5'-GCGCTGCAGGCGGCCGCAGGGCCTGCTAGGGCTAGGAGCGGGGC-3'
corresponding to nt 11-37 of rat mGluR4 cDNA
(Tanabe, et al., (1992), Neuron 8, 169-179)

P4: 5'-GCGGAATTCCCTCCGTGCCGTCCTTCTCG-3'
corresponding to nt 440-459 of rat mGluR4 cDNA
(Tanabe, et al., (1992), Neuron 8, 169-179)

Additional sequences are underlined, sites for restriction enzymes are indicated in boldface.

PCR reactions for a 100 µl reaction mixture are: 400 ng of human genomic DNA, 1 µM of each primer, 2 mM of each deoxynucleoside triphosphate (dATP, dCTP, dGTP and dTTP) in PCR-buffer (10mM Tris-HCl, pH 8.3, 1.5 mM $MgCl_2$, 50 mM KCl, and 2 U AmpliTaq Polymerase. The amplification is performed using the following conditions: 1

min denaturation at 95°C, 1 min annealing at 56°C, and 1 min extension at 72°C, for a total of 32 cycles. Initial denaturation is carried out for 3 min at 94°C.

Products of several independent PCRs are digested with restriction enzymes PstI and EcoRI, gel purified, and ligated into the PstI/EcoRI sites of pBluescript SK (Stratagene). Subcloned fragments of several independent PCRs are analyzed by DNA sequence analysis (cR4PCR1-4). Sequence analysis reveals that clone cR4PCR2 encodes 380 nt of hmGluR4 coding region including the translation initiation codon (nt 1 - 380, cf. SEQ ID NO:1). cR4PCR2 overlaps at the 3' end for 223 nt with cmR20.

The complete deduced amino acid sequence of the hmGluR4 protein is set forth in SEQ ID NO:2.

Example 2: cDNA clones encoding hmGluR7

Screening of human fetal brain and human cerebellum cDNA libraries by low-stringency hybridization using radiolabeled rat mGluR4 fragment (as described in 1.5 and 1.6) allows the isolation of cDNA clones that identify the human metabotropic glutamate receptor subtype mGluR7. Characterization of cDNA clones by DNA sequence analysis reveals that isolated cDNAs represent at least two apparent splice variants of human mGluR7 mRNA.

cDNA cmR2 (isolated from human fetal brain cDNA library) has a size of 3804 nt. Clone cmR2 contains 2604 nt of hmGluR7 coding sequence including a translation termination codon followed by 1200 nt of 3' untranslated sequence (cf. SEQ ID NO:3).

cDNA cmR3 (isolated from human hippocampus cDNA library) has a size of 1399 nt (SEQ ID NO:5). cmR3 contains 270 nt of the hmGluR7 3' end coding region including a translation termination stop codon (the deduced amino acid sequence is set forth in SEQ ID NO:6) followed by 1129 nt of 3' untranslated sequence. The sequence of cmR3 is completely contained in cmR2 but differs from cmR2 by deletion of the 92 nucleotides extending from the nt at position 2534 to the nt at position 2625 in SEQ ID NO:3). This apparent splice variant of hmGluR7 generates a different 3' end of the deduced hmGluR7 amino acid sequence.

cDNA cmR5 (isolated from human fetal brain cDNA library) has a size of 1588 nt (SEQ ID NO:7). cDNA cmR5 overlaps 1424 nt with cDNA cmR2. It diverges at the 3' end exactly at the position of the 92-nt-insertion/deletion of cmR2/cmR3. Additional 164 nt of cmR5 either encode intronic sequences as indicated by presence of a conserved splice

donor sequence immediately following the site of cmR5 and cmR2/cmR3 sequence divergence, or represent a third splice variant.

The 5' end coding region of hmGluR7 DNA missing in cDNA clones cmR2, cmR3, and cmR5, is isolated by a combination of genomic library screening and PCR techniques. A Lamda-Fix genomic library (Stratagene) is screened with a EcoRI/SmaI restriction fragment comprising nt 1-1304 of cDNA cmR2 under high stringency hybridization conditions as described in Sambrook, et al. (1989), supra. Lambda clones hybridizing to the 5' end of cDNA clone cmR2 are purified and analyzed by restriction analyses and DNA sequencing. The complete 5' end of the coding region of human mGluR7 including the ATG translation initiation codon is amplified by PCR from human brain cDNA using primer sequences derived from cloned genomic fragments. The PCR fragments has a size of 557 nt. It is designated as cR7PCR1and depicted as SEQ ID NO:9. The deduced amino acid sequence is set forth in SEQ ID NO:10. cR7PCR1 overlaps at the 3' end with cmR2 for 392 nt.

The DNA sequences coding for the complete hmGluR7a and b proteins are set forth in SEQ ID NOs:11 and 13, respectively. The deduced amino acid sequences are given in SEQ ID NOs:12 and 14, respectively. Comparison of the deduced amino acid sequences reveals approximately 70 % sequence identity to the hmGluR4 subtype of Example 1.

Example 3: cDNA encoding partial hmGluR6

A single cDNA clone, cmR1, with an insert of 1.0 kb is isolated from a human hippocampus library by low stringency hybridization using the hmGluR fragment as described above in example 1.5 and 1.6. Approximately 630 nucleotides are homologous to human mGluR4. Additional sequences at the 5' and 3' end of cmR1 apparently encode intronic sequences as indicated by the presence of putative splice donor and splice acceptor site sequences. cDNA cmR1 identifies a portion of the human metabotropic glutamate receptor subtype hmGluR6 (SEQ ID NOs. 15). The deduced amino acid sequence is set forth in SEQ ID NO:16.

The complete coding region of hmGluR6 is isolated by screening of cDNA and genomic libraries under high stringency conditions with cDNA cmR1 as a probe. Comparison of the deduced amino acid sequences reveals approximately 70% sequence identity to hmGluR4 of Example 1.

Example 4: Expression of hmGluR cDNAs in mammalian cells

4.1 Receptor expression plasmids

cDNAs encoding the above full-length hmGluR4, hmGluR6, and hmGluR7 proteins are generated from cDNA fragments and ligated into mammalian expression vectors based on constitutive promoters (CMV, SV40, RSV) or inducible promoters. Examples are pBK-CMV (Stratagene), pBK-RSV (Stratagene), pCMV-T7 (Sibia, Inc.) and pICP4 (Novagen, USA).

The full-length cDNA encoding the hmGluR4 subtype is incorporated into the mammalian expression vector pBK-CMV by ligating the hmGluR4 5' end fragment (clone cR4PCR2) with cDNA cmR20 at the unique XhoI site that is located at nt 346-351 of the hmGluR4 cDNA. Specifically, plasmid pBK-CMV-hmGluR4 is generated by three-way-ligation of the NotI/XhoI fragment of cR4PCR2, the XhoI/NotI fragment of cDNA cmR20 and the NotI digested vector pBK-CMV. Plasmid pCMV-T7-hmGluR4 is generated by three-way-ligation of the PstI/XhoI fragment of cR4PCR4, the XhoI/EcoRI fragment of cmR20 and the PstI/EcoRI digested vector pCMV-T7-2. Both expression constructs contain the complete coding region of the hmGluR4 as well as approximately 750 nt of 3' untranslated sequences.

Full-length cDNAs representing the two hmGluR7 splice variants, designated hmGluR7a (SEQ ID NO:12) and hmGluR7b SEQ ID NO:14), are incorporated in pCMV-T7-2 (SIBIA Inc.) using the overlapping cDNA clones cmR2, cmR3 and hcR7PCR1. A full-length hmGluR7b expression construct, designated pCMV-T7-hmGluR7b, is prepared by three-way-ligation of the PstI/BsaI fragment of hcR7PCR1, the BsaI/EagI fragment of cmR2 and the PstI/NotI of pCMV-T7-2. Plasmid pCMV-T7-hmGluR7b contains the complete coding region of hmGluR7b and 191 nt of 3' untranslated sequences. To construct a full-length hmGluR7a expression construct, designated pCMV-T7-hmGluR7a, a 370 bp HindIII/EagI fragment of cmR2 is exchanged with the corresponding fragment of cmR3. The BsaI/EagI fragment of the resulting clone is used for a three-way-ligation as describe above.

Plasmid pBK-CMV-hmGluR6 is generated analogously using conventional techniques (Sambrook et al. supra).

4.2 Transfection of mammalian cells

Mammalian cells (e.g. CHO-K1, GH3; American Tissue Type Culture Collection) are

adapted to grow in glutamate free medium (Dulbecco's modified Eagle's medium lacking L-glutamate and containing a reduced concentration of 2 mM L-glutamine, supplemented with 0.046 mg/ml proline and 10% dialyzed fetal bovine serum, Gibco-BRL). HmGluR expression plasmids are transiently transfected into the cells by calcium-phophate precipitation (Ausubel, F. M., et al. (1993) Current Protocols in Molecular Biology, Greene and Wiley, USA).
Cell lines stably expressing hmGluRs are generated by lipofectin-mediated transfection (Gibco-BRL) of CHO-K1 cells with hmGluR expression plasmids and pSV2-Neo (Southern and Berg, 1982), a plasmid vector encoding the G-418 resistence gene. Cells are grown for 48 hours prior to the addition of 1 mg/ml G-418 sulfate (Geneticin, Gibco). Medium is replaced every two to three days. Cells surviving the G-418 selection are isolated and grown in the selection medium. 32 G-418 resistant clonal cell lines are analyzed six to eight weeks after the initial transfection for hmGluR protein expression by immunoreactivity with the anti-hmGluR7 antibody (immunodetection, cf. 4.3, infra) and functional responses following agonist addition via cAMP radioimmunoassay (cf. 5.1, infra).

Likewise, the hmGluR expression constructs pBK-CMV-hmGluR4, pCMV-T7-hmGluR4, pCMV-T7-hmGluR7b and pCMV-T7-hmGluR7a are transiently and stably expressed in mammalian cells (CV1, CHO, HEK293, COS) according to standard procedures (Ausubel, F. M., et al. (1993) Current Protocols in Molecular Biology, Greene and Wiley, USA). The transfected cells are analyzed for hmGluR expression by various assays: [^{3}H]-glutamate binding studies, immunocytochemistry using hmGluR subtype specific antibodies, and assays detecting a change in the intracellular concentration of cAMP ([cAMP]).

4.3 Immunodetection of hmGluR protein expression with subtype-specific hmGluR antibodies

HmGluR protein expression is analyzed by immunocytochemistry with subtype-specific hmGluR antibodies (see Example 7). 1 to 3 days after transfection cells are washed twice with phosphate buffered saline (PBS), fixed with PBS/4% paraformaldehyde for 10 min and washed with PBS. Cells are permeabilized with PBS/0.4 % Triton X-100, followed by washing with PBS/10 mM glycine, and PBS. Cells are blocked with PBSTB (1x PBS/0.1% Triton X-100/1 % BSA) for 1 h and subsequently incubated with immunopurified hmGluR antiserum (0.5 - 2.0 µg/ml in PBSTB) for 1 h. After three washes with PBS, cells are incubated for 1 h with alkaline peroxidase conjugated goat

anti-rabbit IgG (1:200 in PBSTB; Jackson Immuno Research). Cells are washed three times with PBS and immunoreactivity is detected with 0.4 mg/ml naphtolphosphate (Biorad)/1 mg/ml Fast Red (Biorad)/10 mM Levamisole (Sigma)/100 mM Tris/HCl pH 8.8/100 mM NaCl/50 mM $MgCl_2$. The staining reaction is stopped after 15 min by subsequent washing with PBS. 2 to 4 cell lines, each homogenously expressing hmGluR4, hmGluR6 or hmGluR7, are identified by immunostaining.

Example 5: Use of stable cell lines expressing hmGluRs for the screening of modulators of receptor activity

Stable cell lines expressing hmGluR4, hmGluR6 and hmGluR7 are used to screen for agonists, antagonists and allosteric modulators. Such compounds are identified by binding studies employing [^{3}H]glutamate and/or measurement of changes in intracellular second messenger levels ([cAMP], [Ca^{2+}]).

5.1 cAMP radioimmunoassay

Ligand binding and agonist-induced depression of forskolin stimulated cAMP accumulation (changes in the intracellular cAMP concentration) are analyzed by cAMP radioimmunoassay (Amersham). Cells are seeded in 12-well plates at a density of 0.5-2.0 x 10^5 cells per well and grown for 2 to 4 days until a confluent layer of cells is obtained. Cells are washed twice with PBS and incubated for 20 min in PBS containing 1 mM 3-isobutyl-1-methylxanthine (IBMX). Cells are incubated with fresh PBS containing 10 µM forskolin, 1 mM IBMX and a known hmGluR agonist for 20 min. The agonistic effect is stopped and cAMP produced by the cells is released by adding 1 ml of ethanol-water-HCl mix (100 ml of ethanol, 50 ml of water, 1 ml of 1 M HCl) after having aspirated the drug containing medium. cAMP levels are determined by a cAMP radioimmunoassay involving [^{3}H] cAMP (Amersham).

HmGluR subtypes 4, 6 and 7 are negatively coupled to adenylate cyclase when expressed in CHO cells. Agonist binding leads to an inhibition of forskolin induced cAMP accumulation. All subtypes are AP-4 sensitive, meaning that AP 4 has an agonistic effect in a concentration less than 1 mM.

5.2 Measurement of intracellular [Ca^{2+}]

Cells transformed with one of the above expression plasmids are loaded with a calcium sensitive fluorescent dye such as fura-2 or fluro-3. To achieve this cells are plated in single wells, single wells containing a coverslip, or 96-well plates and grown for 1 to 5

days until a 50-100 % confluent layer of cells is obtained. Wells are washed three times with a balance salt solution (BBS) and incubated for 1h in BBS followed by three additional washings with BBS. Then cells are incubated for 20 to 60 min in a solution containing 50 µg fura-2-AM (or fluro3-AM) (Molecular Probes, Inc.) 4.99 ml BBS, 75 µl DMSO and 6.25 µg Pluronic (Molecular Probes, Inc). The cells are washed 3 times with BBS containing 2 mg/ml bovine albumin followed by three washes in BBS. After allowing recovery of the cells for at least 10 min they are used for microfluorometric measurements of $[Ca^{2+}]$.

Cells are transferred to an apparatus for fluometry such as an inverted microscope, a spectrofluometer of a fluorescence reader. Fluorescence of the calcium indicator (e.g. fura-2 or fluo-3) is induced by illumination with light of a wavelength covered by the excitation spectrum of the dye (fura-2: 340/380 nm, fluo-3 3 480 nm). An increase in intracellular free claciom ion concentration is monitored as an increase of fura-2 or fluo-3 fluorescence excited at 340 nm and 480 nm, respectively, or a decrease of fura-2 fluorescence excited at 380 nm.
As a positive control L-glutamate is applied at a concentration corresponding to its EC_{50} value onto the cells, thereby inducing a measurable increase in the intracellular calcium ion concentration. A test compound is said to be an agonist if it induces a Ca^{2+} signal comparable to that induced by glutamate. A test compound is said to be an antagonist if the glutamate induced calcium signal is smaller in the presence of the test compound than in the absence of the test compound.

Example 6: Chimeric hmGluR4, 6 and 7 receptors

Intracellular domains of mGluR1, particularly the second intracellular loop (i2) and the C-terminal region, have been shown to be critical for binding of G-proteins, which activate the phospholipase C/Ca^{2+} signaling pathway, without changing the pharmacological profile of the receptor (Pin et al., EMBO J. 13, 342-348, (1994)). Conventional PCR mutagenesis techniques are used to exchange intracellular domains of hmGluRs 4,6, and 7 with corresponding domains of hmGluR1. Stable CHO cell lines are generated with hmGluR4/1, 6/1 and 7/1 chimeric expression constructs allowing to analyze the influence of modulators of receptor activity (hmGluRs 4,6,7) using Ca^{2+}-dependent assays. In the following, we describe the generation of a chimeric hmGluR7/1 receptor. Expression constructs with chimeric hmGluR4/1 and hmGluR6/1 are generated using analogous cloning and PCR techniques.
(i) The expression construct pCMV-hmGluR7b is digested with EagI, thereby releasing

the complete cDNA insert. The cDNA is cloned into the NotI site of pBluescript-Not, a derivative of pBluescript II (Stratagene) where the polylinker sequences between the unique KpnI and NotI sites are deleted. The resulting clone is designated as pBluescript-Not-hmGluR7.

(ii) The transmembrane region of hmGluR1 is cloned by PCR using primers derived from Masu et al., 1991, supra. The oligonucleotide with the sequence

5'-TATCTTGAGTGGAGTGACATAG-3'

(corresponding to nt 1753 to 1774 of the Masu sequence) is used as sense primer. The antisense primer has the sequence

5'-ACTGCGGACGTTCCTCTCAGG-3'

corresponding to nt 2524 to 2544 of the Masu sequence. The C-terminal end of splice variants 1a, 1b and 1c is cleaved by PCR using primers derived from Masu et al., 1991, Tanabe et al., 1992, supra, and Pin et al., 1992 (Proc. Natl. Acad. Sci, USA, 89, 10331-10335 (1992)), respectively. The oligonucleotide having the sequence

5'-AAACCTGAGAGGAACGTCCGCAG-3'

(corresponding to nt 2521 to nt 2543 of the Masu sequence) is used as sense primer. The oligonucleotides having the sequences

5'-CTACAGGGTGGAAGAGCTTTGCTT-3' corresponding to nt 3577 to 3600 of the Masu sequence,

5'-TCAAAGCTGCGCATGTGCCGACGG-3' corresponding to nt 2698 to 2721 of the Tanabe sequence, and

5'-TCAATAGACAGTGTTTTGGCGGTC-3' corresponding to nt 2671 to 2694 of the Pin sequence are used as antisense primers for hmGluR1a, 1b and 1c, respectively.

The PCR fragment is cloned into pBluescript II and sequenced completely.

(iii) A chimeric cDNA fragment wherein the i2-loop of hmGluR7a or hmGluR7b (nt 2035 to 2106 of SEQ IDs 11 and 13, respectively) is replaced with the corresponding sequences of hmGluR1 is generated by PCR (as described in Pin et al., 1994, supra). The fragment ist digested with SmaI and BglII which cut at unique restriction sites flanking the i2-loop. The chimeric SmaI/BglII fragment is exchanged for the SmaI/BglII fragments of pBluescript-Not-mGluR7.

(iv) Additional replacement of the C-terminal domain of hmGluR7b or hmGluR7a with the corresponding sequences of the above mentioned hmGluR1 splice variants is achieved by using the unique restriction sites BglII and SacII flanking the C-terminal end of hmGluR7.

(v) The resulting chimeric hmGluR7/hmGluR1 cDNAs are sequenced and digested with EagI, thereby releasing the complete cDNAs from pBluescript-Not. For stable expression

in CHO cells, the chimeric cDNAs are cloned into the unique NotI site of the mammalian expression vector pCMV-T7-2.

Example 7: Generation and application of anti-hmGluR antibodies

Peptides corresponding to the deduced C-terminal amino acid sequences of hmGluR4 and hmGluR7 are synthesized and coupled to ovalbumin or Tentagel. Polyclonal antisera are raised in rabbits. Human mGluR specific antibodies are purified from the antisera by immunoaffinity chromatography on peptide columns. The hmGluR specific antibodies are characterized by ELISA and immunoblotting with glutathione-S-transferase/hmGluR fusion proteins (produced in E. coli) or human brain extracts. Antibodies specific for hmGluR4 and hmGluR7, respectively, are used to detect hmGluR receptors in transfected cells and to analyze the cellular and subcellular expression pattern of the hmGluR receptor proteins in tissue sections of human brain material. Antibodies are raised against different hmGluR-specific peptides consisting of 20 amino acids and fusion proteins expressed in E.coli. Peptides are synthesized by solid-phase synthesis, coupled to keyhole limpit hemocyanin (KLH) or ovalbumin with glutaraldehyde. PCR fragments containing the entire putative intracellular C-terminal fragment of hmGluRs are cloned as BamHI/EcoRI fragments into the E. coli expression plasmid pGEX-2T (Guan and Dixon, Analytical Biochemistry 192, 262-267 (1991)) generating glutathione-S-transferase(GST)/hmGluR fusion genes. E. coli DH5a cells (Gibco-BRL) carrying expression plasmids with GST/hmGluR fusion genes are grown overnight at 37°C in LB medium/100 mg/ml ampicillin. The cultures are diluted 1:30 in LB and grown for 2 h at 30°C. Expression of fusion proteins is induced by treatment with 0.1 mM isopropyl-b-D-thiogalactopyranoside for 3 h at 30°C. Cells are harvested by centrifugation at 5,000 x g. The fusion protein is isolated using glutathione affinity chromatography.

Deposition Data

The following plasmids were deposited with the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSM), Mascheroder Weg 1b, D-38124 Braunschweig on September 13, 1993:

Plasmid cmR1; accession no. DSM 8549

Plasmid cmR2; accession no. DSM 8550

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) NAME: CIBA-GEIGY AG
(B) STREET: Klybeckstr. 141
(C) CITY: Basel
(E) COUNTRY: SCHWEIZ
(F) POSTAL CODE (ZIP): 4002
(G) TELEPHONE: +41 61 69 11 11
(H) TELEFAX: + 41 61 696 79 76
(I) TELEX: 962 991

(ii) TITLE OF INVENTION: human receptor proteins

(iii) NUMBER OF SEQUENCES: 16

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2739 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..2739
(D) OTHER INFORMATION: /product= "hmGluR4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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ATG CCT GGG AAG AGA GGC TTG GGC TGG TGG TGG GCC CGG CTG CCC CTT      48
Met Pro Gly Lys Arg Gly Leu Gly Trp Trp Trp Ala Arg Leu Pro Leu
 1               5                  10                  15

TGC CTG CTC CTC AGC CTT TAC GGC CCC TGG ATG CCT TCC TCC CTG GGA      96
Cys Leu Leu Leu Ser Leu Tyr Gly Pro Trp Met Pro Ser Ser Leu Gly
            20                  25                  30

AAG CCC AAA GGC CAC CCT CAC ATG AAT TCC ATC CGC ATA GAT GGG GAC     144
Lys Pro Lys Gly His Pro His Met Asn Ser Ile Arg Ile Asp Gly Asp
        35                  40                  45

ATC ACA CTG GGA GGC CTG TTC CCG GTG CAT GGC CGG GGC TCA GAG GGC     192
Ile Thr Leu Gly Gly Leu Phe Pro Val His Gly Arg Gly Ser Glu Gly
    50                  55                  60

AAG CCC TGT GGA GAA CTT AAG AAG GAA AAG GGC ATC CAC CGG CTG GAG     240
Lys Pro Cys Gly Glu Leu Lys Lys Glu Lys Gly Ile His Arg Leu Glu
65                  70                  75                  80

GCC ATG CTG TTC GCC CTG GAT CGC ATC AAC AAC GAC CCG GAC CTG CTG     288
Ala Met Leu Phe Ala Leu Asp Arg Ile Asn Asn Asp Pro Asp Leu Leu
                85                  90                  95
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CCT AAC ATC ACG CTG GGC GCC CGC ATT CTG GAC ACC TGC TCC AGG GAC      336
Pro Asn Ile Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp
            100                 105                 110

ACC CAT GCC CTC GAG CAG TCG CTG ACC TTT GTG CAG GCG CTC ATC GAG      384
Thr His Ala Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Glu
        115                 120                 125

AAG GAT GGC ACA GAG GTC CGC TGT GGC AGT GGC GGC CCA CCC ATC ATC      432
Lys Asp Gly Thr Glu Val Arg Cys Gly Ser Gly Gly Pro Pro Ile Ile
    130                 135                 140

ACC AAG CCT GAA CGT GTG GTG GGT GTC ATC GGT GCT TCA GGG AGC TCG      480
Thr Lys Pro Glu Arg Val Val Gly Val Ile Gly Ala Ser Gly Ser Ser
145                 150                 155                 160

GTC TCC ATC ATG GTG GCC AAC ATC CTT CGC CTC TTC AAG ATA CCC CAG      528
Val Ser Ile Met Val Ala Asn Ile Leu Arg Leu Phe Lys Ile Pro Gln
                165                 170                 175

ATC AGC TAC GCC TCC ACA GCG CCA GAC CTG AGT GAC AAC AGC CGC TAC      576
Ile Ser Tyr Ala Ser Thr Ala Pro Asp Leu Ser Asp Asn Ser Arg Tyr
            180                 185                 190

GAC TTC TTC TCC CGC GTG GTG CCC TCG GAC ACG TAC CAG GCC CAG GCC      624
Asp Phe Phe Ser Arg Val Val Pro Ser Asp Thr Tyr Gln Ala Gln Ala
        195                 200                 205

ATG GTG GAC ATC GTC CGT GCC CTC AAG TGG AAC TAT GTG TCC ACA GTG      672
Met Val Asp Ile Val Arg Ala Leu Lys Trp Asn Tyr Val Ser Thr Val
    210                 215                 220

GCC TCG GAG GGC AGC TAT GGT GAG AGC GGT GTG GAG GCC TTC ATC CAG      720
Ala Ser Glu Gly Ser Tyr Gly Glu Ser Gly Val Glu Ala Phe Ile Gln
225                 230                 235                 240
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AAG TCC CGT GAG GAC GGG GGC GTG TGC ATC GCC CAG TCG GTG AAG ATA      768
Lys Ser Arg Glu Asp Gly Gly Val Cys Ile Ala Gln Ser Val Lys Ile
                245                 250                 255

CCA CGG GAG CCC AAG GCA GGC GAG TTC GAC AAG ATC ATC CGC CGC CTC      816
Pro Arg Glu Pro Lys Ala Gly Glu Phe Asp Lys Ile Ile Arg Arg Leu
            260                 265                 270

CTG GAG ACT TCG AAC GCC AGG GCA GTC ATC ATC TTT GCC AAC GAG GAT      864
Leu Glu Thr Ser Asn Ala Arg Ala Val Ile Ile Phe Ala Asn Glu Asp
        275                 280                 285

GAC ATC AGG CGT GTG CTG GAG GCA GCA CGA AGG GCC AAC CAG ACA GGC      912
Asp Ile Arg Arg Val Leu Glu Ala Ala Arg Arg Ala Asn Gln Thr Gly
    290                 295                 300

CAT TTC TTC TGG ATG GGC TCT GAC AGC TGG GGC TCC AAG ATT GCA CCT      960
His Phe Phe Trp Met Gly Ser Asp Ser Trp Gly Ser Lys Ile Ala Pro
305                 310                 315                 320

GTG CTG CAC CTG GAG GAG GTG GCT GAG GGT GCT GTC ACG ATC CTC CCC     1008
Val Leu His Leu Glu Glu Val Ala Glu Gly Ala Val Thr Ile Leu Pro
                325                 330                 335

AAG AGG ATG TCC GTA CGA GGC TTC GAC CGC TAC TTC TCC AGC CGC ACG     1056
Lys Arg Met Ser Val Arg Gly Phe Asp Arg Tyr Phe Ser Ser Arg Thr
            340                 345                 350

CTG GAC AAC AAC CGG CGC AAC ATC TGG TTT GCC GAG TTC TGG GAG GAC     1104
Leu Asp Asn Asn Arg Arg Asn Ile Trp Phe Ala Glu Phe Trp Glu Asp
        355                 360                 365

AAC TTC CAC TGC AAG CTG AGC CGC CAC GCC CTC AAG AAG GGC AGC CAC     1152
Asn Phe His Cys Lys Leu Ser Arg His Ala Leu Lys Lys Gly Ser His
    370                 375                 380
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GTC AAG AAG TGC ACC AAC CGT GAG CGA ATT GGG CAG GAT TCA GCT TAT     1200
Val Lys Lys Cys Thr Asn Arg Glu Arg Ile Gly Gln Asp Ser Ala Tyr
385                 390                 395                 400

GAG CAG GAG GGG AAG GTG CAG TTT GTG ATC GAT GCC GTG TAC GCC ATG     1248
Glu Gln Glu Gly Lys Val Gln Phe Val Ile Asp Ala Val Tyr Ala Met
                405                 410                 415

GGC CAC GCG CTG CAC GCC ATG CAC CGT GAC CTG TGT CCC GGC CGC GTG     1296
Gly His Ala Leu His Ala Met His Arg Asp Leu Cys Pro Gly Arg Val
            420                 425                 430

GGG CTC TGC CCG CGC ATG GAC CCT GTA GAT GGC ACC CAG CTG CTT AAG     1344
Gly Leu Cys Pro Arg Met Asp Pro Val Asp Gly Thr Gln Leu Leu Lys
        435                 440                 445

TAC ATC CGA AAC GTC AAC TTC TCA GGC ATC GCA GGG AAC CCT GTG ACC     1392
Tyr Ile Arg Asn Val Asn Phe Ser Gly Ile Ala Gly Asn Pro Val Thr
    450                 455                 460

TTC AAT GAG AAT GGA GAT GCG CCT GGG CGC TAT GAC ATC TAC CAA TAC     1440
Phe Asn Glu Asn Gly Asp Ala Pro Gly Arg Tyr Asp Ile Tyr Gln Tyr
465                 470                 475                 480

CAG CTG CGC AAC GAT TCT GCC GAG TAC AAG GTC ATT GGC TCC TGG ACT     1488
Gln Leu Arg Asn Asp Ser Ala Glu Tyr Lys Val Ile Gly Ser Trp Thr
                485                 490                 495

GAC CAC CTG CAC CTT AGA ATA GAG CGG ATG CAC TGG CCG GGG AGC GGG     1536
Asp His Leu His Leu Arg Ile Glu Arg Met His Trp Pro Gly Ser Gly
            500                 505                 510

CAG CAG CTG CCC CGC TCC ATC TGC AGC CTG CCC TGC CAA CCG GGT GAG     1584
Gln Gln Leu Pro Arg Ser Ile Cys Ser Leu Pro Cys Gln Pro Gly Glu
        515                 520                 525
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CGG AAG AAG ACA GTG AAG GGC ATG CCT TGC TGC TGG CAC TGC GAG CCT      1632
Arg Lys Lys Thr Val Lys Gly Met Pro Cys Cys Trp His Cys Glu Pro
    530                 535                 540

TGC ACA GGG TAC CAG TAC CAG GTG GAC CGC TAC ACC TGT AAG ACG TGT      1680
Cys Thr Gly Tyr Gln Tyr Gln Val Asp Arg Tyr Thr Cys Lys Thr Cys
545                 550                 555                 560

CCC TAT GAC ATG CGG CCC ACA GAG AAC CGC ACG GGC TGC CGG CCC ATC      1728
Pro Tyr Asp Met Arg Pro Thr Glu Asn Arg Thr Gly Cys Arg Pro Ile
                565                 570                 575

CCC ATC ATC AAG CTT GAG TGG GGC TCG CCC TGG GCC GTG CTG CCC CTC      1776
Pro Ile Ile Lys Leu Glu Trp Gly Ser Pro Trp Ala Val Leu Pro Leu
            580                 585                 590

TTC CTG GCC GTG GTG GGC ATC GCT GCC ACG TTG TTC GTG GTG ATC ACC      1824
Phe Leu Ala Val Val Gly Ile Ala Ala Thr Leu Phe Val Val Ile Thr
        595                 600                 605

TTT GTG CGC TAC AAC GAC ACG CCC ATC GTC AAG GCC TCG GGC CGT GAA      1872
Phe Val Arg Tyr Asn Asp Thr Pro Ile Val Lys Ala Ser Gly Arg Glu
    610                 615                 620

CTG AGC TAC GTG CTG CTG GCA GGC ATC TTC CTG TGC TAT GCC ACC ACC      1920
Leu Ser Tyr Val Leu Leu Ala Gly Ile Phe Leu Cys Tyr Ala Thr Thr
625                 630                 635                 640

TTC CTC ATG ATC GCT GAG CCC GAC CTT GGC ACC TGC TCG CTG CGC CGA      1968
Phe Leu Met Ile Ala Glu Pro Asp Leu Gly Thr Cys Ser Leu Arg Arg
                645                 650                 655

ATC TTC CTG GGA CTA GGG ATG AGC ATC AGC TAT GCA GCC CTG CTC ACC      2016
Ile Phe Leu Gly Leu Gly Met Ser Ile Ser Tyr Ala Ala Leu Leu Thr
            660                 665                 670
```

```
AAG ACC AAC CGC ATC TAC CGC ATC TTC GAG CAG GGC AAG CGC TCG GTC     2064
Lys Thr Asn Arg Ile Tyr Arg Ile Phe Glu Gln Gly Lys Arg Ser Val
        675                 680                 685

AGT GCC CCA CGC TTC ATC AGC CCC GCC TCA CAG CTG GCC ATC ACC TTC     2112
Ser Ala Pro Arg Phe Ile Ser Pro Ala Ser Gln Leu Ala Ile Thr Phe
    690                 695                 700

AGC CTC ATC TCG CTG CAG CTG CTG GGC ATC TGT GTG TGG TTT GTG GTG     2160
Ser Leu Ile Ser Leu Gln Leu Leu Gly Ile Cys Val Trp Phe Val Val
705                 710                 715                 720

GAC CCC TCC CAC TCG GTG GTG GAC TTC CAG GAC CAG CGG ACA CTC GAC     2208
Asp Pro Ser His Ser Val Val Asp Phe Gln Asp Gln Arg Thr Leu Asp
                725                 730                 735

CCC CGC TTC GCC AGG GGT GTG CTC AAG TGT GAC ATC TCG GAC CTG TCG     2256
Pro Arg Phe Ala Arg Gly Val Leu Lys Cys Asp Ile Ser Asp Leu Ser
            740                 745                 750

CTC ATC TGC CTG CTG GGC TAC AGC ATG CTG CTC ATG GTC ACG TGC ACC     2304
Leu Ile Cys Leu Leu Gly Tyr Ser Met Leu Leu Met Val Thr Cys Thr
        755                 760                 765

GTG TAT GCC ATC AAG ACA CGC GGC GTG CCC GAG ACC TTC AAT GAG GCC     2352
Val Tyr Ala Ile Lys Thr Arg Gly Val Pro Glu Thr Phe Asn Glu Ala
    770                 775                 780

AAG CCC ATT GGC TTC ACC ATG TAC ACC ACT TGC ATC GTC TGG CTG GCC     2400
Lys Pro Ile Gly Phe Thr Met Tyr Thr Thr Cys Ile Val Trp Leu Ala
785                 790                 795                 800

TTC ATC CCC ATC TTC TTT GGC ACC TCG CAG TCG GCC GAC AAG CTG TAC     2448
Phe Ile Pro Ile Phe Phe Gly Thr Ser Gln Ser Ala Asp Lys Leu Tyr
                805                 810                 815
```

```
ATC CAG ACG ACG ACG CTG ACG GTC TCG GTG AGT CTG AGC GCC TCG GTG     2496
Ile Gln Thr Thr Thr Leu Thr Val Ser Val Ser Leu Ser Ala Ser Val
            820                 825                 830

TCC CTG GGA ATG CTC TAC ATG CCC AAA GTC TAC ATC ATC CTC TTC CAC     2544
Ser Leu Gly Met Leu Tyr Met Pro Lys Val Tyr Ile Ile Leu Phe His
        835                 840                 845

CCG GAG CAG AAC GTG CCC AAG CGC AAG CGC AGC CTC AAA GCC GTC GTT     2592
Pro Glu Gln Asn Val Pro Lys Arg Lys Arg Ser Leu Lys Ala Val Val
    850                 855                 860

ACG GCG GCC ACC ATG TCC AAC AAG TTC ACG CAG AAG GGC AAC TTC CGG     2640
Thr Ala Ala Thr Met Ser Asn Lys Phe Thr Gln Lys Gly Asn Phe Arg
865                 870                 875                 880

CCC AAC GGA GAG GCC AAG TCT GAG CTC TGC GAG AAC CTT GAG GCC CCA     2688
Pro Asn Gly Glu Ala Lys Ser Glu Leu Cys Glu Asn Leu Glu Ala Pro
                885                 890                 895

GCG CTG GCC ACC AAA CAG ACT TAC GTC ACT TAC ACC AAC CAT GCA ATC     2736
Ala Leu Ala Thr Lys Gln Thr Tyr Val Thr Tyr Thr Asn His Ala Ile
            900                 905                 910

TA                                                                  2739
```

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 912 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Pro Gly Lys Arg Gly Leu Gly Trp Trp Trp Ala Arg Leu Pro Leu
 1               5                  10                  15

Cys Leu Leu Leu Ser Leu Tyr Gly Pro Trp Met Pro Ser Ser Leu Gly
            20                  25                  30

Lys Pro Lys Gly His Pro His Met Asn Ser Ile Arg Ile Asp Gly Asp
        35                  40                  45

Ile Thr Leu Gly Gly Leu Phe Pro Val His Gly Arg Gly Ser Glu Gly
    50                  55                  60

Lys Pro Cys Gly Glu Leu Lys Lys Glu Lys Gly Ile His Arg Leu Glu
65                  70                  75                  80

Ala Met Leu Phe Ala Leu Asp Arg Ile Asn Asn Asp Pro Asp Leu Leu
                85                  90                  95

Pro Asn Ile Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp
            100                 105                 110

Thr His Ala Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Glu
        115                 120                 125

Lys Asp Gly Thr Glu Val Arg Cys Gly Ser Gly Gly Pro Pro Ile Ile
    130                 135                 140

Thr Lys Pro Glu Arg Val Val Gly Val Ile Gly Ala Ser Gly Ser Ser
145                 150                 155                 160

Val Ser Ile Met Val Ala Asn Ile Leu Arg Leu Phe Lys Ile Pro Gln
                165                 170                 175
```

```
Ile Ser Tyr Ala Ser Thr Ala Pro Asp Leu Ser Asp Asn Ser Arg Tyr
            180                 185                 190

Asp Phe Phe Ser Arg Val Val Pro Ser Asp Thr Tyr Gln Ala Gln Ala
        195                 200                 205

Met Val Asp Ile Val Arg Ala Leu Lys Trp Asn Tyr Val Ser Thr Val
    210                 215                 220

Ala Ser Glu Gly Ser Tyr Gly Glu Ser Gly Val Glu Ala Phe Ile Gln
225                 230                 235                 240

Lys Ser Arg Glu Asp Gly Gly Val Cys Ile Ala Gln Ser Val Lys Ile
                245                 250                 255

Pro Arg Glu Pro Lys Ala Gly Glu Phe Asp Lys Ile Ile Arg Arg Leu
            260                 265                 270

Leu Glu Thr Ser Asn Ala Arg Ala Val Ile Ile Phe Ala Asn Glu Asp
        275                 280                 285

Asp Ile Arg Arg Val Leu Glu Ala Ala Arg Arg Ala Asn Gln Thr Gly
    290                 295                 300

His Phe Phe Trp Met Gly Ser Asp Ser Trp Gly Ser Lys Ile Ala Pro
305                 310                 315                 320

Val Leu His Leu Glu Glu Val Ala Glu Gly Ala Val Thr Ile Leu Pro
                325                 330                 335

Lys Arg Met Ser Val Arg Gly Phe Asp Arg Tyr Phe Ser Ser Arg Thr
            340                 345                 350

Leu Asp Asn Asn Arg Arg Asn Ile Trp Phe Ala Glu Phe Trp Glu Asp
        355                 360                 365
```

```
Asn Phe His Cys Lys Leu Ser Arg His Ala Leu Lys Lys Gly Ser His
    370                 375                 380

Val Lys Lys Cys Thr Asn Arg Glu Arg Ile Gly Gln Asp Ser Ala Tyr
385                 390                 395                 400

Glu Gln Glu Gly Lys Val Gln Phe Val Ile Asp Ala Val Tyr Ala Met
                405                 410                 415

Gly His Ala Leu His Ala Met His Arg Asp Leu Cys Pro Gly Arg Val
            420                 425                 430

Gly Leu Cys Pro Arg Met Asp Pro Val Asp Gly Thr Gln Leu Leu Lys
        435                 440                 445

Tyr Ile Arg Asn Val Asn Phe Ser Gly Ile Ala Gly Asn Pro Val Thr
    450                 455                 460

Phe Asn Glu Asn Gly Asp Ala Pro Gly Arg Tyr Asp Ile Tyr Gln Tyr
465                 470                 475                 480

Gln Leu Arg Asn Asp Ser Ala Glu Tyr Lys Val Ile Gly Ser Trp Thr
                485                 490                 495

Asp His Leu His Leu Arg Ile Glu Arg Met His Trp Pro Gly Ser Gly
            500                 505                 510

Gln Gln Leu Pro Arg Ser Ile Cys Ser Leu Pro Cys Gln Pro Gly Glu
        515                 520                 525

Arg Lys Lys Thr Val Lys Gly Met Pro Cys Cys Trp His Cys Glu Pro
    530                 535                 540

Cys Thr Gly Tyr Gln Tyr Gln Val Asp Arg Tyr Thr Cys Lys Thr Cys
545                 550                 555                 560
```

```
Pro Tyr Asp Met Arg Pro Thr Glu Asn Arg Thr Gly Cys Arg Pro Ile
                565                 570                 575

Pro Ile Ile Lys Leu Glu Trp Gly Ser Pro Trp Ala Val Leu Pro Leu
            580                 585                 590

Phe Leu Ala Val Val Gly Ile Ala Ala Thr Leu Phe Val Val Ile Thr
        595                 600                 605

Phe Val Arg Tyr Asn Asp Thr Pro Ile Val Lys Ala Ser Gly Arg Glu
    610                 615                 620

Leu Ser Tyr Val Leu Leu Ala Gly Ile Phe Leu Cys Tyr Ala Thr Thr
625                 630                 635                 640

Phe Leu Met Ile Ala Glu Pro Asp Leu Gly Thr Cys Ser Leu Arg Arg
                645                 650                 655

Ile Phe Leu Gly Leu Gly Met Ser Ile Ser Tyr Ala Ala Leu Leu Thr
            660                 665                 670

Lys Thr Asn Arg Ile Tyr Arg Ile Phe Glu Gln Gly Lys Arg Ser Val
        675                 680                 685

Ser Ala Pro Arg Phe Ile Ser Pro Ala Ser Gln Leu Ala Ile Thr Phe
    690                 695                 700

Ser Leu Ile Ser Leu Gln Leu Leu Gly Ile Cys Val Trp Phe Val Val
705                 710                 715                 720

Asp Pro Ser His Ser Val Val Asp Phe Gln Asp Gln Arg Thr Leu Asp
                725                 730                 735

Pro Arg Phe Ala Arg Gly Val Leu Lys Cys Asp Ile Ser Asp Leu Ser
            740                 745                 750
```

Leu Ile Cys Leu Leu Gly Tyr Ser Met Leu Leu Met Val Thr Cys Thr
755 760 765

Val Tyr Ala Ile Lys Thr Arg Gly Val Pro Glu Thr Phe Asn Glu Ala
770 775 780

Lys Pro Ile Gly Phe Thr Met Tyr Thr Thr Cys Ile Val Trp Leu Ala
785 790 795 800

Phe Ile Pro Ile Phe Phe Gly Thr Ser Gln Ser Ala Asp Lys Leu Tyr
805 810 815

Ile Gln Thr Thr Thr Leu Thr Val Ser Val Ser Leu Ser Ala Ser Val
820 825 830

Ser Leu Gly Met Leu Tyr Met Pro Lys Val Tyr Ile Ile Leu Phe His
835 840 845

Pro Glu Gln Asn Val Pro Lys Arg Lys Arg Ser Leu Lys Ala Val Val
850 855 860

Thr Ala Ala Thr Met Ser Asn Lys Phe Thr Gln Lys Gly Asn Phe Arg
865 870 875 880

Pro Asn Gly Glu Ala Lys Ser Glu Leu Cys Glu Asn Leu Glu Ala Pro
885 890 895

Ala Leu Ala Thr Lys Gln Thr Tyr Val Thr Tyr Thr Asn His Ala Ile
900 905 910

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3804 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..2604
(D) OTHER INFORMATION: /product= "hmGluR7 encoding region of cmR2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
CCC GTA CAC GCC AAG GGT CCC AGC GGA GTG CCC TGC GGC GAC ATC AAG      48
Pro Val His Ala Lys Gly Pro Ser Gly Val Pro Cys Gly Asp Ile Lys
 1               5                  10                  15

AGG GAA AAC GGG ATC CAC AGG CTG GAA GCG ATG CTC TAC GCC CTG GAC      96
Arg Glu Asn Gly Ile His Arg Leu Glu Ala Met Leu Tyr Ala Leu Asp
            20                  25                  30

CAG ATC AAC AGT GAT CCC AAC CTA CTG CCC AAC GTG ACG CTG GGC GCG     144
Gln Ile Asn Ser Asp Pro Asn Leu Leu Pro Asn Val Thr Leu Gly Ala
        35                  40                  45
```

```
CGG ATC CTG GAC ACT TGT TCC AGG GAC ACT TAC GCG CTC GAA CAG TCG      192
Arg Ile Leu Asp Thr Cys Ser Arg Asp Thr Tyr Ala Leu Glu Gln Ser
     50                  55                  60

CTT ACT TTC GTC CAG GCG CTC ATC CAG AAG GAC ACC TCC GAC GTG CGC      240
Leu Thr Phe Val Gln Ala Leu Ile Gln Lys Asp Thr Ser Asp Val Arg
 65                  70                  75                  80

TGC ACC AAC GGC GAA CCG CCG GTT TTC GTC AAG CCG GAG AAA GTA GTT      288
Cys Thr Asn Gly Glu Pro Pro Val Phe Val Lys Pro Glu Lys Val Val
                85                  90                  95

GGA GTG ATT GGG GCT TCG GGG AGT TCG GTC TCC ATC ATG GTA GCC AAC      336
Gly Val Ile Gly Ala Ser Gly Ser Ser Val Ser Ile Met Val Ala Asn
            100                 105                 110

ATC CTG AGG CTC TTC CAG ATC CCC CAG ATT AGT TAT GCA TCA ACG GCA      384
Ile Leu Arg Leu Phe Gln Ile Pro Gln Ile Ser Tyr Ala Ser Thr Ala
        115                 120                 125

CCC GAG CTA AGT GAT GAC CGG CGC TAT GAC TTC TTC TCT CGC GTG GTG      432
Pro Glu Leu Ser Asp Asp Arg Arg Tyr Asp Phe Phe Ser Arg Val Val
    130                 135                 140

CCA CCC GAT TCC TTC CAA GCC CAG GCC ATG GTA GAC ATT GTA AAG GCC      480
Pro Pro Asp Ser Phe Gln Ala Gln Ala Met Val Asp Ile Val Lys Ala
145                 150                 155                 160

CTA GGC TGG AAT TAT GTG TCT ACC CTC GCA TCG GAA GGA AGT TAT GGA      528
Leu Gly Trp Asn Tyr Val Ser Thr Leu Ala Ser Glu Gly Ser Tyr Gly
                165                 170                 175

GAG AAA GGT GTG GAG TCC TTC ACG CAG ATT TCC AAA GAG GCA GGT GGA      576
Glu Lys Gly Val Glu Ser Phe Thr Gln Ile Ser Lys Glu Ala Gly Gly
            180                 185                 190
```

```
CTC TGC ATT GCC CAG TCC GTG AGA ATC CCC CAG GAA CGC AAA GAC AGG      624
Leu Cys Ile Ala Gln Ser Val Arg Ile Pro Gln Glu Arg Lys Asp Arg
        195                 200                 205

ACC ATT GAC TTT GAT AGA ATT ATC AAA CAG CTC CTG GAC ACC CCC AAC      672
Thr Ile Asp Phe Asp Arg Ile Ile Lys Gln Leu Leu Asp Thr Pro Asn
    210                 215                 220

TCC AGG GCC GTC GTG ATT TTT GCC AAC GAT GAG GAT ATA AAG CAG ATC      720
Ser Arg Ala Val Val Ile Phe Ala Asn Asp Glu Asp Ile Lys Gln Ile
225                 230                 235                 240

CTT GCA GCA GCC AAA AGA GCT GAC CAA GTT GGC CAT TTT CTT TGG GTG      768
Leu Ala Ala Ala Lys Arg Ala Asp Gln Val Gly His Phe Leu Trp Val
                245                 250                 255

GGA TCA GAC AGC TGG GGA TCC AAA ATA AAC CCA CTG CAC CAG CAT GAA      816
Gly Ser Asp Ser Trp Gly Ser Lys Ile Asn Pro Leu His Gln His Glu
            260                 265                 270

GAT ATC GCA GAA GGG GCC ATC ACC ATT CAG CCC AAG CGA GCC ACG GTG      864
Asp Ile Ala Glu Gly Ala Ile Thr Ile Gln Pro Lys Arg Ala Thr Val
        275                 280                 285

GAA GGG TTT GAT GCC TAC TTT ACG TCC CGT ACA CTT GAA AAC AAC AGA      912
Glu Gly Phe Asp Ala Tyr Phe Thr Ser Arg Thr Leu Glu Asn Asn Arg
    290                 295                 300

AGA AAT GTA TGG TTT GCC GAA TAC TGG GAG GAA AAC TTC AAC TGC AAG      960
Arg Asn Val Trp Phe Ala Glu Tyr Trp Glu Glu Asn Phe Asn Cys Lys
305                 310                 315                 320

TTG ACG ATT AGT GGG TCA AAA AAA GAA GAC ACA GAT CGC AAA TGC ACA     1008
Leu Thr Ile Ser Gly Ser Lys Lys Glu Asp Thr Asp Arg Lys Cys Thr
                325                 330                 335
```

```
GGA CAG GAG AGA ATT GGA AAA GAT TCC AAC TAT GAG CAG GAG GGT AAA     1056
Gly Gln Glu Arg Ile Gly Lys Asp Ser Asn Tyr Glu Gln Glu Gly Lys
            340                 345                 350

GTC CAG TTC GTG ATT GAC GCA GTC TAT GCT ATG GCT CAC GCC CTT CAC     1104
Val Gln Phe Val Ile Asp Ala Val Tyr Ala Met Ala His Ala Leu His
        355                 360                 365

CAC ATG AAC AAG GAT CTC TGT GCT GAC TAC CGG GGT GTC TGC CCA GAG     1152
His Met Asn Lys Asp Leu Cys Ala Asp Tyr Arg Gly Val Cys Pro Glu
    370                 375                 380

ATG GAG CAA GCT GGA GGC AAG AAG TTG CTG AAG TAT ATA CGC AAT GTT     1200
Met Glu Gln Ala Gly Gly Lys Lys Leu Leu Lys Tyr Ile Arg Asn Val
385                 390                 395                 400

AAT TTC AAT GGT AGT GCT GGC ACT CCA GTG ATG TTT AAC AAG AAC GGG     1248
Asn Phe Asn Gly Ser Ala Gly Thr Pro Val Met Phe Asn Lys Asn Gly
            405                 410                 415

GAT GCA CCT GGG CGT TAT GAC ATC TTT CAG TAC CAG ACC ACA AAC ACC     1296
Asp Ala Pro Gly Arg Tyr Asp Ile Phe Gln Tyr Gln Thr Thr Asn Thr
            420                 425                 430

AGC AAC CCG GGT TAC CGT CTG ATC GGG CAG TGG ACA GAC GAA CTT CAG     1344
Ser Asn Pro Gly Tyr Arg Leu Ile Gly Gln Trp Thr Asp Glu Leu Gln
        435                 440                 445

CTC AAT ATA GAA GAC ATG CAG TGG GGT AAA GGA GTC CGA GAG ATA CCC     1392
Leu Asn Ile Glu Asp Met Gln Trp Gly Lys Gly Val Arg Glu Ile Pro
    450                 455                 460

GCC TCA GTG TGC ACA CTA CCA TGT AAG CCA GGA CAG AGA AAG AAG ACA     1440
Ala Ser Val Cys Thr Leu Pro Cys Lys Pro Gly Gln Arg Lys Lys Thr
465                 470                 475                 480
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```
CAG AAA GGA ACT CCT TGC TGT TGG ACC TGT GAG CCT TGC GAT GGT TAC     1488
Gln Lys Gly Thr Pro Cys Cys Trp Thr Cys Glu Pro Cys Asp Gly Tyr
                485                 490                 495

CAG TAC CAG TTT GAT GAG ATG ACA TGC CAG CAT TGC CCC TAT GAC CAG     1536
Gln Tyr Gln Phe Asp Glu Met Thr Cys Gln His Cys Pro Tyr Asp Gln
            500                 505                 510

AGG CCC AAT GAA AAT CGA ACC GGA TGC CAG GAT ATT CCC ATC ATC AAA     1584
Arg Pro Asn Glu Asn Arg Thr Gly Cys Gln Asp Ile Pro Ile Ile Lys
        515                 520                 525

CTG GAG TGG CAC TCC CCC TGG GCT GTG ATT CCT GTC TTC CTG GCA ATG     1632
Leu Glu Trp His Ser Pro Trp Ala Val Ile Pro Val Phe Leu Ala Met
    530                 535                 540

TTG GGG ATC ATT GCC ACC ATC TTT GTC ATG GCC ACT TTC ATC CGC TAC     1680
Leu Gly Ile Ile Ala Thr Ile Phe Val Met Ala Thr Phe Ile Arg Tyr
545                 550                 555                 560

AAT GAC ACG CCC ATT GTC CGG GCA TCT GGG CGG GAA CTC AGC TAT GTT     1728
Asn Asp Thr Pro Ile Val Arg Ala Ser Gly Arg Glu Leu Ser Tyr Val
                565                 570                 575

CTT TTG ACG GGC ATC TTT CTT TGC TAC ATC ATC ACT TTC CTG ATG ATT     1776
Leu Leu Thr Gly Ile Phe Leu Cys Tyr Ile Ile Thr Phe Leu Met Ile
            580                 585                 590

GCC AAA CCA GAT GTG GCA GTG TGT TCT TTC CGG CGA GTT TTC TTG GGC     1824
Ala Lys Pro Asp Val Ala Val Cys Ser Phe Arg Arg Val Phe Leu Gly
        595                 600                 605

TTG GGT ATG TGC ATC AGT TAT GCA GCC CTC TTG ACG AAA ACA AAT CGG     1872
Leu Gly Met Cys Ile Ser Tyr Ala Ala Leu Leu Thr Lys Thr Asn Arg
    610                 615                 620
```

```
ATT TAT CGC ATA TTT GAG CAG GGC AAG AAA TCA GTA ACA GCT CCC AGA     1920
Ile Tyr Arg Ile Phe Glu Gln Gly Lys Lys Ser Val Thr Ala Pro Arg
625                 630                 635                 640

CTC ATA AGC CCA ACA TCA CAA CTG GCA ATC ACT TCC AGT TTA ATA TCA     1968
Leu Ile Ser Pro Thr Ser Gln Leu Ala Ile Thr Ser Ser Leu Ile Ser
                645                 650                 655

GTT CAG CTT CTA GGG GTG TTC ATT TGG TTT GGT GTT GAT CCA CCC AAC     2016
Val Gln Leu Leu Gly Val Phe Ile Trp Phe Gly Val Asp Pro Pro Asn
            660                 665                 670

ATC ATC ATA GAC TAC GAT GAA CAC AAG ACA ATG AAC CCT GAG CAA GCC     2064
Ile Ile Ile Asp Tyr Asp Glu His Lys Thr Met Asn Pro Glu Gln Ala
        675                 680                 685

AGA GGG GTT CTC AAG TGT GAC ATT ACA GAT CTC CAA ATC ATT TGC TCC     2112
Arg Gly Val Leu Lys Cys Asp Ile Thr Asp Leu Gln Ile Ile Cys Ser
    690                 695                 700

TTG GGA TAT AGC ATT CTT CTC ATG GTC ACA TGT ACT GTG TAT GCC ATC     2160
Leu Gly Tyr Ser Ile Leu Leu Met Val Thr Cys Thr Val Tyr Ala Ile
705                 710                 715                 720

AAG ACT CGG GGT GTA CCC GAG AAT TTT AAC GAA GCC AAG CCC ATT GGA     2208
Lys Thr Arg Gly Val Pro Glu Asn Phe Asn Glu Ala Lys Pro Ile Gly
                725                 730                 735

TTC ACT ATG TAC ACG ACA TGT ATA GTA TGG CTT GCC TTC ATT CCA ATT     2256
Phe Thr Met Tyr Thr Thr Cys Ile Val Trp Leu Ala Phe Ile Pro Ile
            740                 745                 750

TTT TTT GGC ACC GCT CAA TCA GCG GAA AAG CTC TAC ATA CAA ACT ACC     2304
Phe Phe Gly Thr Ala Gln Ser Ala Glu Lys Leu Tyr Ile Gln Thr Thr
        755                 760                 765
```

```
ACG CTT ACA ATC TCC ATG AAC CTA AGT GCA TCA GTG GCG CTG GGG ATG     2352
Thr Leu Thr Ile Ser Met Asn Leu Ser Ala Ser Val Ala Leu Gly Met
    770                 775                 780

CTA TAC ATG CCG AAA GTG TAC ATC ATC ATT TTC CAC CCT GAA CTC AAT     2400
Leu Tyr Met Pro Lys Val Tyr Ile Ile Ile Phe His Pro Glu Leu Asn
785                 790                 795                 800

GTC CAG AAA CGG AAG CGA AGC TTC AAG GCG GTA GTC ACA GCA GCC ACC     2448
Val Gln Lys Arg Lys Arg Ser Phe Lys Ala Val Val Thr Ala Ala Thr
                805                 810                 815

ATG TCA TCG AGG CTG TCA CAC AAA CCC AGT GAC AGA CCC AAC GGT GAG     2496
Met Ser Ser Arg Leu Ser His Lys Pro Ser Asp Arg Pro Asn Gly Glu
            820                 825                 830

GCA AAG ACC GAG CTC TGT GAA AAC GTA GAC CCA AAC AAC TGT ATA CCA     2544
Ala Lys Thr Glu Leu Cys Glu Asn Val Asp Pro Asn Asn Cys Ile Pro
        835                 840                 845

CCA GTA AGA AAG AGT GTA CAA AAG TCT GTT ACT TGG TAC ACT ATC CCA     2592
Pro Val Arg Lys Ser Val Gln Lys Ser Val Thr Trp Tyr Thr Ile Pro
    850                 855                 860

CCA ACA GTA TAGCTTTTGA CTGCTTTCCC AAAGGCCCTG CTGCAAAAAA             2641
Pro Thr Val
865

GAAGTATGTC AGTTATAATA ACCTGGTTAT CTAACCTGTT CCATTCCATG GAACCATGGA   2701

GGAGGAAGAC CCTCAGTTAT TTTGTCACCC AACCTGGCAT AGGACTCTTT GGTCCTACCC   2761

GCTTCCCATC ACCGGAGGAG CTTCCCCGGC CGGGAGACCA GTGTTAGAGG ATCCAAGCGA   2821

CCTAAACAGC TGCTTTATGA AATATCCTTA CTTTATCTGG GCTTAATAAG TCACTGACAT   2881
```

CAGCACTGCC AACTTGGCTG CAATTGTGGA CCTTCCCTAC CAAAGGGAGT GTTGAAACTC 2941

AAGTCCCGCC CCGGCTCTTT AGAATGGACC ACTGAGAGCC ACAGGACCGT TTTGGGGCTG 3001

ACCTGTCTTA TTACGTATGT ACTTCTAGGT TGCAAGGTTT TGAAATTTTC TGTACAGTTT 3061

GTGAGGACCT TTGCACTTTG CCATCTGATG TCGTACCTCG GTTCACTGTT TGTTTTCGAA 3121

TGCCTTGTTT TCATAGAGCC CTATTCTCTC AGACGGTGGA ATATTTGGAA AAATTTTAAA 3181

ACAATTAAAA TTTTAAAGCA ATCTTGGCAG ACTAAAACAA GTACATCTGT ACATGACTGT 3241

ATAATTACGT TATAGTACCA CTGCACATCA TGTTTTTTTT TTTAAGACAA AAAAGATGTT 3301

TAAAGACCAA AAACTGTGCT GAGNAAGTAT GCCCCACCTA TCTTTNGNAT ATGATAGGTT 3361

ACATAAAAGG AAGGTATTGG CTGAACTGNA TAGAGGTCTT GATCTTTGGA ATGCATGCCA 3421

GTAATGTATT TACAGTACAT GTTTATTATG TTCAATATTT GTATTTGTGT TCTCTTTTGT 3481

TATTTTTAAT TAGNGTATAT GAATATTTTG CAATAATTTT AATAATTATT AAGCTGTTTG 3541

AAGGAAAGAA TATGGATTTT TCATGTCTTG AGGTTTTGTT CATGCCCCCT TTGACTGATC 3601

AGTGTGATAA GGACTTTAGG AAAAAAAGCA TGTATGTTTT TTACTGTTTG TAATAAGTAC 3661

TTTCGTTAAT CTTGCTGCTT ATGTGCCAAT TTAGTGGAAA AGAACAACCC TTGCTGAAAA 3721

ATTCCCTCTT TCCATTCTCT TTCAATTCTG TGATATTGTC CAAGAATGTA TCAATAAAAT 3781

ACTTTGGTTA ACTTTAAAAA AAA 3804

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 867 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```
Pro Val His Ala Lys Gly Pro Ser Gly Val Pro Cys Gly Asp Ile Lys
 1               5                  10                  15

Arg Glu Asn Gly Ile His Arg Leu Glu Ala Met Leu Tyr Ala Leu Asp
            20                  25                  30

Gln Ile Asn Ser Asp Pro Asn Leu Leu Pro Asn Val Thr Leu Gly Ala
        35                  40                  45

Arg Ile Leu Asp Thr Cys Ser Arg Asp Thr Tyr Ala Leu Glu Gln Ser
    50                  55                  60

Leu Thr Phe Val Gln Ala Leu Ile Gln Lys Asp Thr Ser Asp Val Arg
65                  70                  75                  80

Cys Thr Asn Gly Glu Pro Pro Val Phe Val Lys Pro Glu Lys Val Val
                85                  90                  95

Gly Val Ile Gly Ala Ser Gly Ser Ser Val Ser Ile Met Val Ala Asn
            100                 105                 110

Ile Leu Arg Leu Phe Gln Ile Pro Gln Ile Ser Tyr Ala Ser Thr Ala
        115                 120                 125
```

```
Pro Glu Leu Ser Asp Asp Arg Arg Tyr Asp Phe Phe Ser Arg Val Val
    130                 135                 140

Pro Pro Asp Ser Phe Gln Ala Gln Ala Met Val Asp Ile Val Lys Ala
145                 150                 155                 160

Leu Gly Trp Asn Tyr Val Ser Thr Leu Ala Ser Glu Gly Ser Tyr Gly
                165                 170                 175

Glu Lys Gly Val Glu Ser Phe Thr Gln Ile Ser Lys Glu Ala Gly Gly
            180                 185                 190

Leu Cys Ile Ala Gln Ser Val Arg Ile Pro Gln Glu Arg Lys Asp Arg
        195                 200                 205

Thr Ile Asp Phe Asp Arg Ile Ile Lys Gln Leu Leu Asp Thr Pro Asn
    210                 215                 220

Ser Arg Ala Val Val Ile Phe Ala Asn Asp Glu Asp Ile Lys Gln Ile
225                 230                 235                 240

Leu Ala Ala Ala Lys Arg Ala Asp Gln Val Gly His Phe Leu Trp Val
                245                 250                 255

Gly Ser Asp Ser Trp Gly Ser Lys Ile Asn Pro Leu His Gln His Glu
            260                 265                 270

Asp Ile Ala Glu Gly Ala Ile Thr Ile Gln Pro Lys Arg Ala Thr Val
        275                 280                 285

Glu Gly Phe Asp Ala Tyr Phe Thr Ser Arg Thr Leu Glu Asn Asn Arg
    290                 295                 300

Arg Asn Val Trp Phe Ala Glu Tyr Trp Glu Glu Asn Phe Asn Cys Lys
305                 310                 315                 320
```

```
Leu Thr Ile Ser Gly Ser Lys Lys Glu Asp Thr Asp Arg Lys Cys Thr
                325                 330                 335

Gly Gln Glu Arg Ile Gly Lys Asp Ser Asn Tyr Glu Gln Glu Gly Lys
            340                 345                 350

Val Gln Phe Val Ile Asp Ala Val Tyr Ala Met Ala His Ala Leu His
        355                 360                 365

His Met Asn Lys Asp Leu Cys Ala Asp Tyr Arg Gly Val Cys Pro Glu
    370                 375                 380

Met Glu Gln Ala Gly Gly Lys Lys Leu Leu Lys Tyr Ile Arg Asn Val
385                 390                 395                 400

Asn Phe Asn Gly Ser Ala Gly Thr Pro Val Met Phe Asn Lys Asn Gly
                405                 410                 415

Asp Ala Pro Gly Arg Tyr Asp Ile Phe Gln Tyr Gln Thr Thr Asn Thr
            420                 425                 430

Ser Asn Pro Gly Tyr Arg Leu Ile Gly Gln Trp Thr Asp Glu Leu Gln
        435                 440                 445

Leu Asn Ile Glu Asp Met Gln Trp Gly Lys Gly Val Arg Glu Ile Pro
    450                 455                 460

Ala Ser Val Cys Thr Leu Pro Cys Lys Pro Gly Gln Arg Lys Lys Thr
465                 470                 475                 480

Gln Lys Gly Thr Pro Cys Cys Trp Thr Cys Glu Pro Cys Asp Gly Tyr
                485                 490                 495

Gln Tyr Gln Phe Asp Glu Met Thr Cys Gln His Cys Pro Tyr Asp Gln
            500                 505                 510
```

Arg Pro Asn Glu Asn Arg Thr Gly Cys Gln Asp Ile Pro Ile Ile Lys
515 520 525

Leu Glu Trp His Ser Pro Trp Ala Val Ile Pro Val Phe Leu Ala Met
530 535 540

Leu Gly Ile Ile Ala Thr Ile Phe Val Met Ala Thr Phe Ile Arg Tyr
545 550 555 560

Asn Asp Thr Pro Ile Val Arg Ala Ser Gly Arg Glu Leu Ser Tyr Val
565 570 575

Leu Leu Thr Gly Ile Phe Leu Cys Tyr Ile Ile Thr Phe Leu Met Ile
580 585 590

Ala Lys Pro Asp Val Ala Val Cys Ser Phe Arg Arg Val Phe Leu Gly
595 600 605

Leu Gly Met Cys Ile Ser Tyr Ala Ala Leu Leu Thr Lys Thr Asn Arg
610 615 620

Ile Tyr Arg Ile Phe Glu Gln Gly Lys Lys Ser Val Thr Ala Pro Arg
625 630 635 640

Leu Ile Ser Pro Thr Ser Gln Leu Ala Ile Thr Ser Ser Leu Ile Ser
645 650 655

Val Gln Leu Leu Gly Val Phe Ile Trp Phe Gly Val Asp Pro Pro Asn
660 665 670

Ile Ile Ile Asp Tyr Asp Glu His Lys Thr Met Asn Pro Glu Gln Ala
675 680 685

Arg Gly Val Leu Lys Cys Asp Ile Thr Asp Leu Gln Ile Ile Cys Ser
690 695 700

Leu Gly Tyr Ser Ile Leu Leu Met Val Thr Cys Thr Val Tyr Ala Ile
705 710 715 720

Lys Thr Arg Gly Val Pro Glu Asn Phe Asn Glu Ala Lys Pro Ile Gly
725 730 735

Phe Thr Met Tyr Thr Thr Cys Ile Val Trp Leu Ala Phe Ile Pro Ile
740 745 750

Phe Phe Gly Thr Ala Gln Ser Ala Glu Lys Leu Tyr Ile Gln Thr Thr
755 760 765

Thr Leu Thr Ile Ser Met Asn Leu Ser Ala Ser Val Ala Leu Gly Met
770 775 780

Leu Tyr Met Pro Lys Val Tyr Ile Ile Ile Phe His Pro Glu Leu Asn
785 790 795 800

Val Gln Lys Arg Lys Arg Ser Phe Lys Ala Val Val Thr Ala Ala Thr
805 810 815

Met Ser Ser Arg Leu Ser His Lys Pro Ser Asp Arg Pro Asn Gly Glu
820 825 830

Ala Lys Thr Glu Leu Cys Glu Asn Val Asp Pro Asn Asn Cys Ile Pro
835 840 845

Pro Val Arg Lys Ser Val Gln Lys Ser Val Thr Trp Tyr Thr Ile Pro
850 855 860

Pro Thr Val
865

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..270
(D) OTHER INFORMATION: /product= "hmGluR7 encoding region of cmR3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```
ATC TCC ATG AAC CTA AGT GCA TCA GTG GCG CTG GGG ATG CTA TAC ATG      48
Ile Ser Met Asn Leu Ser Ala Ser Val Ala Leu Gly Met Leu Tyr Met
 1               5                  10                  15

CCG AAA GTG TAC ATC ATC ATT TTC CAC CCT GAA CTC AAT GTC CAG AAA      96
Pro Lys Val Tyr Ile Ile Ile Phe His Pro Glu Leu Asn Val Gln Lys
            20                  25                  30

CGG AAG CGA AGC TTC AAG GCG GTA GTC ACA GCA GCC ACC ATG TCA TCG     144
Arg Lys Arg Ser Phe Lys Ala Val Val Thr Ala Ala Thr Met Ser Ser
        35                  40                  45

AGG CTG TCA CAC AAA CCC AGT GAC AGA CCC AAC GGT GAG GCA AAG ACC     192
Arg Leu Ser His Lys Pro Ser Asp Arg Pro Asn Gly Glu Ala Lys Thr
    50                  55                  60
```

GAG CTC TGT GAA AAC GTA GAC CCA AAC AGC CCT GCT GCA AAA AAG AAG 240
Glu Leu Cys Glu Asn Val Asp Pro Asn Ser Pro Ala Ala Lys Lys Lys
65 70 75 80

TAT GTC AGT TAT AAT AAC CTG GTT ATC TAACCTGTTC CATTCCATGG 287
Tyr Val Ser Tyr Asn Asn Leu Val Ile
85 90

AACCATGGAG GAGGAAGACC CTCAGTTATT TTGTCACCCA ACCTGGCATA GGACTCTTTG 347

GTCCTACCCG CTTCCCATCA CCGGAGGAGC TTCCCCGGCC GGGAGACCAG TGTTAGAGGA 407

TCCAAGCGAC CTAAACAGCT GCTTTATGAA ATATCCTTAC TTTATCTGGG CTTAATAAGT 467

CACTGACATC AGCACTGCCA ACTTGGCTGC AATTGTGGAC CTTCCCTACC AAAGGGAGTG 527

TTGAAACTCA AGTCCCGCCC CGGCTCTTTA GAATGGACCA CTGAGAGCCA CAGGACCGTT 587

TTGGGGCTGA CCTGTCTTAT TACGTATGTA CTTCTAGGTT GCAAGGTTTT GAAATTTTCT 647

GTACAGTTTG TGAGGACCTT TGCACTTTGC CATCTGATGT CGTACCTCGG TTCACTGTTT 707

GTTTTCGAAT GCCTTGTTTT CATAGAGCCC TATTCTCTCA GACGGTGGAA TATTTGGAAA 767

AATTTTAAAA CAATTAAAAT TTTAAAGCAA TCTTGGCAGA CTAAAACAAG TACATCTGTA 827

CATGACTGTA TAATTACGTT ATAGTACCAC TGCACATCAT GTTTTTTTTT TTAAGACAAA 887

AAAGATGTTT AAAGACCAAA AACTGTGCTG AGNAAGTATG CCCCACCTAT CTTTNGNATA 947

TGATAGGTTA CATAAAAGGA AGGTATTGGC TGAACTGNAT AGAGGTCTTG ATCTTTGGAA 1007

TGCATGCCAG TAATGTATTT ACAGTACATG TTTATTATGT TCAATATTTG TATTTGTGTT 1067

CTCTTTTGTT ATTTTTAATT AGNGTATATG AATATTTTGC AATAATTTTA ATAATTATTA 1127

AGCTGTTTGA AGGAAAGAAT ATGGATTTTT CATGTCTTGA GGTTTTGTTC ATGCCCCCTT 1187

TGACTGATCA GTGTGATAAG GACTTTAGGA AAAAAAGCAT GTATGTTTTT TACTGTTTGT 1247

AATAAGTACT TTCGTTAATC TTGCTGCTTA TGTGCCAATT TAGTGGAAAA GAACAACCCT 1307

TGCTGAAAAA TTCCCTCTTT CCATTCTCTT TCAATTCTGT GATATTGTCC AAGAATGTAT 1367

CAATAAAATA CTTTGGTTAA CTTTAAAAAA AA 1399

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Ile Ser Met Asn Leu Ser Ala Ser Val Ala Leu Gly Met Leu Tyr Met
1 5 10 15

Pro Lys Val Tyr Ile Ile Ile Phe His Pro Glu Leu Asn Val Gln Lys
20 25 30

Arg Lys Arg Ser Phe Lys Ala Val Val Thr Ala Ala Thr Met Ser Ser
35 40 45

Arg Leu Ser His Lys Pro Ser Asp Arg Pro Asn Gly Glu Ala Lys Thr
50 55 60

Glu Leu Cys Glu Asn Val Asp Pro Asn Ser Pro Ala Ala Lys Lys Lys
65 70 75 80

Tyr Val Ser Tyr Asn Asn Leu Val Ile
85

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1588 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..1447
(D) OTHER INFORMATION: /product= "hmGluR7 encoding portion of cmR5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```
G AAC AAG GAT CTC TGT GCT GAC TAC CGG GGT GTC TGC CCA GAG ATG      46
  Asn Lys Asp Leu Cys Ala Asp Tyr Arg Gly Val Cys Pro Glu Met
    1               5                  10                  15

GAG CAA GCT GGA GGC AAG AAG TTG CTG AAG TAT ATA CGC AAT GTT AAT    94
Glu Gln Ala Gly Gly Lys Lys Leu Leu Lys Tyr Ile Arg Asn Val Asn
                  20                  25                  30

TTC AAT GGT AGT GCT GGC ACT CCA GTG ATG TTT AAC AAG AAC GGG GAT   142
Phe Asn Gly Ser Ala Gly Thr Pro Val Met Phe Asn Lys Asn Gly Asp
            35                  40                  45
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GCA CCT GGG CGT TAT GAC ATC TTT CAG TAC CAG ACC ACA AAC ACC AGC      190
Ala Pro Gly Arg Tyr Asp Ile Phe Gln Tyr Gln Thr Thr Asn Thr Ser
         50                  55                  60

AAC CCG GGT TAC CGT CTG ATC GGG CAG TGG ACA GAC GAA CTT CAG CTC      238
Asn Pro Gly Tyr Arg Leu Ile Gly Gln Trp Thr Asp Glu Leu Gln Leu
     65                  70                  75

AAT ATA GAA GAC ATG CAG TGG GGT AAA GGA GTC CGA GAG ATA CCC GCC      286
Asn Ile Glu Asp Met Gln Trp Gly Lys Gly Val Arg Glu Ile Pro Ala
 80                  85                  90                  95

TCA GTG TGC ACA CTA CCA TGT AAG CCA GGA CAG AGA AAG AAG ACA CAG      334
Ser Val Cys Thr Leu Pro Cys Lys Pro Gly Gln Arg Lys Lys Thr Gln
                100                 105                 110

AAA GGA ACT CCT TGC TGT TGG ACC TGT GAG CCT TGC GAT GGT TAC CAG      382
Lys Gly Thr Pro Cys Cys Trp Thr Cys Glu Pro Cys Asp Gly Tyr Gln
            115                 120                 125

TAC CAG TTT GAT GAG ATG ACA TGC CAG CAT TGC CCC TAT GAC CAG AGG      430
Tyr Gln Phe Asp Glu Met Thr Cys Gln His Cys Pro Tyr Asp Gln Arg
        130                 135                 140

CCC AAT GAA AAT CGA ACC GGA TGC CAG GAT ATT CCC ATC ATC AAA CTG      478
Pro Asn Glu Asn Arg Thr Gly Cys Gln Asp Ile Pro Ile Ile Lys Leu
    145                 150                 155

GAG TGG CAC TCC CCC TGG GCT GTG ATT CCT GTC TTC CTG GCA ATG TTG      526
Glu Trp His Ser Pro Trp Ala Val Ile Pro Val Phe Leu Ala Met Leu
160                 165                 170                 175

GGG ATC ATT GCC ACC ATC TTT GTC ATG GCC ACT TTC ATC CGC TAC AAT      574
Gly Ile Ile Ala Thr Ile Phe Val Met Ala Thr Phe Ile Arg Tyr Asn
                180                 185                 190
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GAC ACG CCC ATT GTC CGG GCA TCT GGG CGG GAA CTC AGC TAT GTT CTT      622
Asp Thr Pro Ile Val Arg Ala Ser Gly Arg Glu Leu Ser Tyr Val Leu
            195                 200                 205

TTG ACG GGC ATC TTT CTT TGC TAC ATC ATC ACT TTC CTG ATG ATT GCC      670
Leu Thr Gly Ile Phe Leu Cys Tyr Ile Ile Thr Phe Leu Met Ile Ala
        210                 215                 220

AAA CCA GAT GTG GCA GTG TGT TCT TTC CGG CGA GTT TTC TTG GGC TTG      718
Lys Pro Asp Val Ala Val Cys Ser Phe Arg Arg Val Phe Leu Gly Leu
    225                 230                 235

GGT ATG TGC ATC AGT TAT GCA GCC CTC TTG ACG AAA ACA AAT CGG ATT      766
Gly Met Cys Ile Ser Tyr Ala Ala Leu Leu Thr Lys Thr Asn Arg Ile
240                 245                 250                 255

TAT CGC ATA TTT GAG CAG GGC AAG AAA TCA GTA ACA GCT CCC AGA CTC      814
Tyr Arg Ile Phe Glu Gln Gly Lys Lys Ser Val Thr Ala Pro Arg Leu
                260                 265                 270

ATA AGC CCA ACA TCA CAA CTG GCA ATC ACT TCC AGT TTA ATA TCA GTT      862
Ile Ser Pro Thr Ser Gln Leu Ala Ile Thr Ser Ser Leu Ile Ser Val
            275                 280                 285

CAG CTT CTA GGG GTG TTC ATT TGG TTT GGT GTT GAT CCA CCC AAC ATC      910
Gln Leu Leu Gly Val Phe Ile Trp Phe Gly Val Asp Pro Pro Asn Ile
        290                 295                 300

ATC ATA GAC TAC GAT GAA CAC AAG ACA ATG AAC CCT GAG CAA GCC AGA      958
Ile Ile Asp Tyr Asp Glu His Lys Thr Met Asn Pro Glu Gln Ala Arg
    305                 310                 315

GGG GTT CTC AAG TGT GAC ATT ACA GAT CTC CAA ATC ATT TGC TCC TTG     1006
Gly Val Leu Lys Cys Asp Ile Thr Asp Leu Gln Ile Ile Cys Ser Leu
320                 325                 330                 335
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```
GGA TAT AGC ATT CTT CTC ATG GTC ACA TGT ACT GTG TAT GCC ATC AAG     1054
Gly Tyr Ser Ile Leu Leu Met Val Thr Cys Thr Val Tyr Ala Ile Lys
                340                 345                 350

ACT CGG GGT GTA CCC GAG AAT TTT AAC GAA GCC AAG CCC ATT GGA TTC     1102
Thr Arg Gly Val Pro Glu Asn Phe Asn Glu Ala Lys Pro Ile Gly Phe
            355                 360                 365

ACT ATG TAC ACG ACA TGT ATA GTA TGG CTT GCC TTC ATT CCA ATT TTT     1150
Thr Met Tyr Thr Thr Cys Ile Val Trp Leu Ala Phe Ile Pro Ile Phe
        370                 375                 380

TTT GGC ACC GCT CAA TCA GCG GAA AAG CTC TAC ATA CAA ACT ACC ACG     1198
Phe Gly Thr Ala Gln Ser Ala Glu Lys Leu Tyr Ile Gln Thr Thr Thr
    385                 390                 395

CTT ACA ATC TCC ATG AAC CTA AGT GCA TCA GTG GCG CTG GGG ATG CTA     1246
Leu Thr Ile Ser Met Asn Leu Ser Ala Ser Val Ala Leu Gly Met Leu
400                 405                 410                 415

TAC ATG CCG AAA GTG TAC ATC ATC ATT TTC CAC CCT GAA CTC AAT GTC     1294
Tyr Met Pro Lys Val Tyr Ile Ile Ile Phe His Pro Glu Leu Asn Val
                420                 425                 430

CAG AAA CGG AAG CGA AGC TTC AAG GCG GTA GTC ACA GCA GCC ACC ATG     1342
Gln Lys Arg Lys Arg Ser Phe Lys Ala Val Val Thr Ala Ala Thr Met
            435                 440                 445

TCA TCG AGG CTG TCA CAC AAA CCC AGT GAC AGA CCC AAC GGT GAG GCA     1390
Ser Ser Arg Leu Ser His Lys Pro Ser Asp Arg Pro Asn Gly Glu Ala
        450                 455                 460

AAG ACC GAG CTC TGT GAA AAC GTA GAC CCA AAC AGT GAG AAG TGC AAC     1438
Lys Thr Glu Leu Cys Glu Asn Val Asp Pro Asn Ser Glu Lys Cys Asn
    465                 470                 475
```

TGC TAC TGACCATCTG CACTGGCATC TAGTCAAGCG ATTGTCTGAG GAAAGGATTT 1494
Cys Tyr
480

TGGAGATTCC CATCTGATAT TCTTCTATTT GGTCTCTTGT ACCCATTGTC ATCCTGTACC 1554

ACACATAATA AAGTTTAAGA ATGTCAAGCA AAAG 1588

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 481 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Asn Lys Asp Leu Cys Ala Asp Tyr Arg Gly Val Cys Pro Glu Met Glu
1 5 10 15

Gln Ala Gly Gly Lys Lys Leu Leu Lys Tyr Ile Arg Asn Val Asn Phe
20 25 30

Asn Gly Ser Ala Gly Thr Pro Val Met Phe Asn Lys Asn Gly Asp Ala
35 40 45

Pro Gly Arg Tyr Asp Ile Phe Gln Tyr Gln Thr Thr Asn Thr Ser Asn
50 55 60

Pro Gly Tyr Arg Leu Ile Gly Gln Trp Thr Asp Glu Leu Gln Leu Asn
65 70 75 80

```
Ile Glu Asp Met Gln Trp Gly Lys Gly Val Arg Glu Ile Pro Ala Ser
                85                  90                  95

Val Cys Thr Leu Pro Cys Lys Pro Gly Gln Arg Lys Lys Thr Gln Lys
            100                 105                 110

Gly Thr Pro Cys Cys Trp Thr Cys Glu Pro Cys Asp Gly Tyr Gln Tyr
        115                 120                 125

Gln Phe Asp Glu Met Thr Cys Gln His Cys Pro Tyr Asp Gln Arg Pro
    130                 135                 140

Asn Glu Asn Arg Thr Gly Cys Gln Asp Ile Pro Ile Ile Lys Leu Glu
145                 150                 155                 160

Trp His Ser Pro Trp Ala Val Ile Pro Val Phe Leu Ala Met Leu Gly
                165                 170                 175

Ile Ile Ala Thr Ile Phe Val Met Ala Thr Phe Ile Arg Tyr Asn Asp
            180                 185                 190

Thr Pro Ile Val Arg Ala Ser Gly Arg Glu Leu Ser Tyr Val Leu Leu
        195                 200                 205

Thr Gly Ile Phe Leu Cys Tyr Ile Ile Thr Phe Leu Met Ile Ala Lys
    210                 215                 220

Pro Asp Val Ala Val Cys Ser Phe Arg Arg Val Phe Leu Gly Leu Gly
225                 230                 235                 240

Met Cys Ile Ser Tyr Ala Ala Leu Leu Thr Lys Thr Asn Arg Ile Tyr
                245                 250                 255

Arg Ile Phe Glu Gln Gly Lys Lys Ser Val Thr Ala Pro Arg Leu Ile
            260                 265                 270
```

Ser Pro Thr Ser Gln Leu Ala Ile Thr Ser Ser Leu Ile Ser Val Gln
275 280 285

Leu Leu Gly Val Phe Ile Trp Phe Gly Val Asp Pro Pro Asn Ile Ile
290 295 300

Ile Asp Tyr Asp Glu His Lys Thr Met Asn Pro Glu Gln Ala Arg Gly
305 310 315 320

Val Leu Lys Cys Asp Ile Thr Asp Leu Gln Ile Ile Cys Ser Leu Gly
325 330 335

Tyr Ser Ile Leu Leu Met Val Thr Cys Thr Val Tyr Ala Ile Lys Thr
340 345 350

Arg Gly Val Pro Glu Asn Phe Asn Glu Ala Lys Pro Ile Gly Phe Thr
355 360 365

Met Tyr Thr Thr Cys Ile Val Trp Leu Ala Phe Ile Pro Ile Phe Phe
370 375 380

Gly Thr Ala Gln Ser Ala Glu Lys Leu Tyr Ile Gln Thr Thr Thr Leu
385 390 395 400

Thr Ile Ser Met Asn Leu Ser Ala Ser Val Ala Leu Gly Met Leu Tyr
405 410 415

Met Pro Lys Val Tyr Ile Ile Ile Phe His Pro Glu Leu Asn Val Gln
420 425 430

Lys Arg Lys Arg Ser Phe Lys Ala Val Val Thr Ala Ala Thr Met Ser
435 440 445

Ser Arg Leu Ser His Lys Pro Ser Asp Arg Pro Asn Gly Glu Ala Lys
450 455 460

Thr Glu Leu Cys Glu Asn Val Asp Pro Asn Ser Glu Lys Cys Asn Cys
465 470 475 480

Tyr

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 558 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..558
(D) OTHER INFORMATION: /product= "hmGluR7 encoding portion of cR7PCR1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATG GTC CAG CTG AGG AAG CTG CTC CGC GTC CTG ACT TTG ATG AAG TTC 48
Met Val Gln Leu Arg Lys Leu Leu Arg Val Leu Thr Leu Met Lys Phe
1 5 10 15

CCC TGC TGC GTG CTG GAG GTG CTC CTG TGC GCG CTG GCG GCG GCG GCG 96
Pro Cys Cys Val Leu Glu Val Leu Leu Cys Ala Leu Ala Ala Ala Ala
20 25 30

```
CGC GGC CAG GAG ATG TAC GCC CCG CAC TCA ATC CGG ATC GAG GGG GAC      144
Arg Gly Gln Glu Met Tyr Ala Pro His Ser Ile Arg Ile Glu Gly Asp
        35                  40                  45

GTC ACC CTC GGG GGG CTG TTC CCC GTA CAC GCC AAG GGT CCC AGC GGA      192
Val Thr Leu Gly Gly Leu Phe Pro Val His Ala Lys Gly Pro Ser Gly
    50                  55                  60

GTG CCC TGC GGC GAC ATC AAG AGG GAA AAC GGG ATC CAC AGG CTG GAA      240
Val Pro Cys Gly Asp Ile Lys Arg Glu Asn Gly Ile His Arg Leu Glu
65                  70                  75                  80

GCG ATG CTC TAC GCC CTG GAC CAG ATC AAC AGT GAT CCC AAC CTA CTG      288
Ala Met Leu Tyr Ala Leu Asp Gln Ile Asn Ser Asp Pro Asn Leu Leu
                85                  90                  95

CCC AAC GTG ACG CTG GGC GCG CGG ATC CTG GAC ACT TGT TCC AGG GAC      336
Pro Asn Val Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp
            100                 105                 110

ACT TAC GCG CTC GAA CAG TCG CTT ACT TTC GTC CAG GCG CTC ATC CAG      384
Thr Tyr Ala Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Gln
        115                 120                 125

AAG GAC ACC TCC GAC GTG CGC TGC ACC AAC GGC GAA CCG CCG GTT TTC      432
Lys Asp Thr Ser Asp Val Arg Cys Thr Asn Gly Glu Pro Pro Val Phe
    130                 135                 140

GTC AAG CCG GAG AAA GTA GTT GGA GTG ATT GGG GCT TCG GGG AGT TCG      480
Val Lys Pro Glu Lys Val Val Gly Val Ile Gly Ala Ser Gly Ser Ser
145                 150                 155                 160

GTC TCC ATC ATG GTA GCC AAC ATC CTG AGG CTC TTC CAG ATC CCC CAG      528
Val Ser Ile Met Val Ala Asn Ile Leu Arg Leu Phe Gln Ile Pro Gln
                165                 170                 175
```

ATT AGT TAT GCA TCA ACG GCA CCC GAG CTA 558
Ile Ser Tyr Ala Ser Thr Ala Pro Glu Leu
180 185

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Val Gln Leu Arg Lys Leu Leu Arg Val Leu Thr Leu Met Lys Phe
1 5 10 15

Pro Cys Cys Val Leu Glu Val Leu Leu Cys Ala Leu Ala Ala Ala Ala
20 25 30

Arg Gly Gln Glu Met Tyr Ala Pro His Ser Ile Arg Ile Glu Gly Asp
35 40 45

Val Thr Leu Gly Gly Leu Phe Pro Val His Ala Lys Gly Pro Ser Gly
50 55 60

Val Pro Cys Gly Asp Ile Lys Arg Glu Asn Gly Ile His Arg Leu Glu
65 70 75 80

Ala Met Leu Tyr Ala Leu Asp Gln Ile Asn Ser Asp Pro Asn Leu Leu
85 90 95

Pro Asn Val Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp
100 105 110

Thr Tyr Ala Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Gln
115 120 125

Lys Asp Thr Ser Asp Val Arg Cys Thr Asn Gly Glu Pro Pro Val Phe
130 135 140

Val Lys Pro Glu Lys Val Val Gly Val Ile Gly Ala Ser Gly Ser Ser
145 150 155 160

Val Ser Ile Met Val Ala Asn Ile Leu Arg Leu Phe Gln Ile Pro Gln
165 170 175

Ile Ser Tyr Ala Ser Thr Ala Pro Glu Leu
180 185

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2748 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..2748
(D) OTHER INFORMATION: /product= "hmGluR7a"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATG GTC CAG CTG AGG AAG CTG CTC CGC GTC CTG ACT TTG ATG AAG TTC 48

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Met Val Gln Leu Arg Lys Leu Leu Arg Val Leu Thr Leu Met Lys Phe
 1               5                  10                  15

CCC TGC TGC GTG CTG GAG GTG CTC CTG TGC GCG CTG GCG GCG GCG GCG      96
Pro Cys Cys Val Leu Glu Val Leu Leu Cys Ala Leu Ala Ala Ala Ala
            20                  25                  30

CGC GGC CAG GAG ATG TAC GCC CCG CAC TCA ATC CGG ATC GAG GGG GAC     144
Arg Gly Gln Glu Met Tyr Ala Pro His Ser Ile Arg Ile Glu Gly Asp
        35                  40                  45

GTC ACC CTC GGG GGG CTG TTC CCC GTA CAC GCC AAG GGT CCC AGC GGA     192
Val Thr Leu Gly Gly Leu Phe Pro Val His Ala Lys Gly Pro Ser Gly
    50                  55                  60

GTG CCC TGC GGC GAC ATC AAG AGG GAA AAC GGG ATC CAC AGG CTG GAA     240
Val Pro Cys Gly Asp Ile Lys Arg Glu Asn Gly Ile His Arg Leu Glu
65                  70                  75                  80

GCG ATG CTC TAC GCC CTG GAC CAG ATC AAC AGT GAT CCC AAC CTA CTG     288
Ala Met Leu Tyr Ala Leu Asp Gln Ile Asn Ser Asp Pro Asn Leu Leu
                85                  90                  95

CCC AAC GTG ACG CTG GGC GCG CGG ATC CTG GAC ACT TGT TCC AGG GAC     336
Pro Asn Val Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp
            100                 105                 110

ACT TAC GCG CTC GAA CAG TCG CTT ACT TTC GTC CAG GCG CTC ATC CAG     384
Thr Tyr Ala Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Gln
        115                 120                 125

AAG GAC ACC TCC GAC GTG CGC TGC ACC AAC GGC GAA CCG CCG GTT TTC     432
Lys Asp Thr Ser Asp Val Arg Cys Thr Asn Gly Glu Pro Pro Val Phe
    130                 135                 140
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GTC AAG CCG GAG AAA GTA GTT GGA GTG ATT GGG GCT TCG GGG AGT TCG      480
Val Lys Pro Glu Lys Val Val Gly Val Ile Gly Ala Ser Gly Ser Ser
145                 150                 155                 160

GTC TCC ATC ATG GTA GCC AAC ATC CTG AGG CTC TTC CAG ATC CCC CAG      528
Val Ser Ile Met Val Ala Asn Ile Leu Arg Leu Phe Gln Ile Pro Gln
                165                 170                 175

ATT AGT TAT GCA TCA ACG GCA CCC GAG CTA AGT GAT GAC CGG CGC TAT      576
Ile Ser Tyr Ala Ser Thr Ala Pro Glu Leu Ser Asp Asp Arg Arg Tyr
            180                 185                 190

GAC TTC TTC TCT CGC GTG GTG CCA CCC GAT TCC TTC CAA GCC CAG GCC      624
Asp Phe Phe Ser Arg Val Val Pro Pro Asp Ser Phe Gln Ala Gln Ala
        195                 200                 205

ATG GTA GAC ATT GTA AAG GCC CTA GGC TGG AAT TAT GTG TCT ACC CTC      672
Met Val Asp Ile Val Lys Ala Leu Gly Trp Asn Tyr Val Ser Thr Leu
    210                 215                 220

GCA TCG GAA GGA AGT TAT GGA GAG AAA GGT GTG GAG TCC TTC ACG CAG      720
Ala Ser Glu Gly Ser Tyr Gly Glu Lys Gly Val Glu Ser Phe Thr Gln
225                 230                 235                 240

ATT TCC AAA GAG GCA GGT GGA CTC TGC ATT GCC CAG TCC GTG AGA ATC      768
Ile Ser Lys Glu Ala Gly Gly Leu Cys Ile Ala Gln Ser Val Arg Ile
                245                 250                 255

CCC CAG GAA CGC AAA GAC AGG ACC ATT GAC TTT GAT AGA ATT ATC AAA      816
Pro Gln Glu Arg Lys Asp Arg Thr Ile Asp Phe Asp Arg Ile Ile Lys
            260                 265                 270

CAG CTC CTG GAC ACC CCC AAC TCC AGG GCC GTC GTG ATT TTT GCC AAC      864
Gln Leu Leu Asp Thr Pro Asn Ser Arg Ala Val Val Ile Phe Ala Asn
        275                 280                 285
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GAT GAG GAT ATA AAG CAG ATC CTT GCA GCA GCC AAA AGA GCT GAC CAA      912
Asp Glu Asp Ile Lys Gln Ile Leu Ala Ala Ala Lys Arg Ala Asp Gln
    290                 295                 300

GTT GGC CAT TTT CTT TGG GTG GGA TCA GAC AGC TGG GGA TCC AAA ATA      960
Val Gly His Phe Leu Trp Val Gly Ser Asp Ser Trp Gly Ser Lys Ile
305                 310                 315                 320

AAC CCA CTG CAC CAG CAT GAA GAT ATC GCA GAA GGG GCC ATC ACC ATT     1008
Asn Pro Leu His Gln His Glu Asp Ile Ala Glu Gly Ala Ile Thr Ile
                325                 330                 335

CAG CCC AAG CGA GCC ACG GTG GAA GGG TTT GAT GCC TAC TTT ACG TCC     1056
Gln Pro Lys Arg Ala Thr Val Glu Gly Phe Asp Ala Tyr Phe Thr Ser
            340                 345                 350

CGT ACA CTT GAA AAC AAC AGA AGA AAT GTA TGG TTT GCC GAA TAC TGG     1104
Arg Thr Leu Glu Asn Asn Arg Arg Asn Val Trp Phe Ala Glu Tyr Trp
        355                 360                 365

GAG GAA AAC TTC AAC TGC AAG TTG ACG ATT AGT GGG TCA AAA AAA GAA     1152
Glu Glu Asn Phe Asn Cys Lys Leu Thr Ile Ser Gly Ser Lys Lys Glu
    370                 375                 380

GAC ACA GAT CGC AAA TGC ACA GGA CAG GAG AGA ATT GGA AAA GAT TCC     1200
Asp Thr Asp Arg Lys Cys Thr Gly Gln Glu Arg Ile Gly Lys Asp Ser
385                 390                 395                 400

AAC TAT GAG CAG GAG GGT AAA GTC CAG TTC GTG ATT GAC GCA GTC TAT     1248
Asn Tyr Glu Gln Glu Gly Lys Val Gln Phe Val Ile Asp Ala Val Tyr
                405                 410                 415

GCT ATG GCT CAC GCC CTT CAC CAC ATG AAC AAG GAT CTC TGT GCT GAC     1296
Ala Met Ala His Ala Leu His His Met Asn Lys Asp Leu Cys Ala Asp
            420                 425                 430
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TAC CGG GGT GTC TGC CCA GAG ATG GAG CAA GCT GGA GGC AAG AAG TTG     1344
Tyr Arg Gly Val Cys Pro Glu Met Glu Gln Ala Gly Gly Lys Lys Leu
        435                 440                 445

CTG AAG TAT ATA CGC AAT GTT AAT TTC AAT GGT AGT GCT GGC ACT CCA     1392
Leu Lys Tyr Ile Arg Asn Val Asn Phe Asn Gly Ser Ala Gly Thr Pro
    450                 455                 460

GTG ATG TTT AAC AAG AAC GGG GAT GCA CCT GGG CGT TAT GAC ATC TTT     1440
Val Met Phe Asn Lys Asn Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe
465                 470                 475                 480

CAG TAC CAG ACC ACA AAC ACC AGC AAC CCG GGT TAC CGT CTG ATC GGG     1488
Gln Tyr Gln Thr Thr Asn Thr Ser Asn Pro Gly Tyr Arg Leu Ile Gly
                485                 490                 495

CAG TGG ACA GAC GAA CTT CAG CTC AAT ATA GAA GAC ATG CAG TGG GGT     1536
Gln Trp Thr Asp Glu Leu Gln Leu Asn Ile Glu Asp Met Gln Trp Gly
            500                 505                 510

AAA GGA GTC CGA GAG ATA CCC GCC TCA GTG TGC ACA CTA CCA TGT AAG     1584
Lys Gly Val Arg Glu Ile Pro Ala Ser Val Cys Thr Leu Pro Cys Lys
        515                 520                 525

CCA GGA CAG AGA AAG AAG ACA CAG AAA GGA ACT CCT TGC TGT TGG ACC     1632
Pro Gly Gln Arg Lys Lys Thr Gln Lys Gly Thr Pro Cys Cys Trp Thr
    530                 535                 540

TGT GAG CCT TGC GAT GGT TAC CAG TAC CAG TTT GAT GAG ATG ACA TGC     1680
Cys Glu Pro Cys Asp Gly Tyr Gln Tyr Gln Phe Asp Glu Met Thr Cys
545                 550                 555                 560

CAG CAT TGC CCC TAT GAC CAG AGG CCC AAT GAA AAT CGA ACC GGA TGC     1728
Gln His Cys Pro Tyr Asp Gln Arg Pro Asn Glu Asn Arg Thr Gly Cys
                565                 570                 575
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```
CAG GAT ATT CCC ATC ATC AAA CTG GAG TGG CAC TCC CCC TGG GCT GTG      1776
Gln Asp Ile Pro Ile Ile Lys Leu Glu Trp His Ser Pro Trp Ala Val
            580                 585                 590

ATT CCT GTC TTC CTG GCA ATG TTG GGG ATC ATT GCC ACC ATC TTT GTC      1824
Ile Pro Val Phe Leu Ala Met Leu Gly Ile Ile Ala Thr Ile Phe Val
        595                 600                 605

ATG GCC ACT TTC ATC CGC TAC AAT GAC ACG CCC ATT GTC CGG GCA TCT      1872
Met Ala Thr Phe Ile Arg Tyr Asn Asp Thr Pro Ile Val Arg Ala Ser
    610                 615                 620

GGG CGG GAA CTC AGC TAT GTT CTT TTG ACG GGC ATC TTT CTT TGC TAC      1920
Gly Arg Glu Leu Ser Tyr Val Leu Leu Thr Gly Ile Phe Leu Cys Tyr
625                 630                 635                 640

ATC ATC ACT TTC CTG ATG ATT GCC AAA CCA GAT GTG GCA GTG TGT TCT      1968
Ile Ile Thr Phe Leu Met Ile Ala Lys Pro Asp Val Ala Val Cys Ser
                645                 650                 655

TTC CGG CGA GTT TTC TTG GGC TTG GGT ATG TGC ATC AGT TAT GCA GCC      2016
Phe Arg Arg Val Phe Leu Gly Leu Gly Met Cys Ile Ser Tyr Ala Ala
            660                 665                 670

CTC TTG ACG AAA ACA AAT CGG ATT TAT CGC ATA TTT GAG CAG GGC AAG      2064
Leu Leu Thr Lys Thr Asn Arg Ile Tyr Arg Ile Phe Glu Gln Gly Lys
        675                 680                 685

AAA TCA GTA ACA GCT CCC AGA CTC ATA AGC CCA ACA TCA CAA CTG GCA      2112
Lys Ser Val Thr Ala Pro Arg Leu Ile Ser Pro Thr Ser Gln Leu Ala
    690                 695                 700

ATC ACT TCC AGT TTA ATA TCA GTT CAG CTT CTA GGG GTG TTC ATT TGG      2160
Ile Thr Ser Ser Leu Ile Ser Val Gln Leu Leu Gly Val Phe Ile Trp
705                 710                 715                 720
```

```
TTT GGT GTT GAT CCA CCC AAC ATC ATC ATA GAC TAC GAT GAA CAC AAG      2208
Phe Gly Val Asp Pro Pro Asn Ile Ile Ile Asp Tyr Asp Glu His Lys
                725                 730                 735

ACA ATG AAC CCT GAG CAA GCC AGA GGG GTT CTC AAG TGT GAC ATT ACA      2256
Thr Met Asn Pro Glu Gln Ala Arg Gly Val Leu Lys Cys Asp Ile Thr
            740                 745                 750

GAT CTC CAA ATC ATT TGC TCC TTG GGA TAT AGC ATT CTT CTC ATG GTC      2304
Asp Leu Gln Ile Ile Cys Ser Leu Gly Tyr Ser Ile Leu Leu Met Val
        755                 760                 765

ACA TGT ACT GTG TAT GCC ATC AAG ACT CGG GGT GTA CCC GAG AAT TTT      2352
Thr Cys Thr Val Tyr Ala Ile Lys Thr Arg Gly Val Pro Glu Asn Phe
    770                 775                 780

AAC GAA GCC AAG CCC ATT GGA TTC ACT ATG TAC ACG ACA TGT ATA GTA      2400
Asn Glu Ala Lys Pro Ile Gly Phe Thr Met Tyr Thr Thr Cys Ile Val
785                 790                 795                 800

TGG CTT GCC TTC ATT CCA ATT TTT TTT GGC ACC GCT CAA TCA GCG GAA      2448
Trp Leu Ala Phe Ile Pro Ile Phe Phe Gly Thr Ala Gln Ser Ala Glu
                805                 810                 815

AAG CTC TAC ATA CAA ACT ACC ACG CTT ACA ATC TCC ATG AAC CTA AGT      2496
Lys Leu Tyr Ile Gln Thr Thr Thr Leu Thr Ile Ser Met Asn Leu Ser
            820                 825                 830

GCA TCA GTG GCG CTG GGG ATG CTA TAC ATG CCG AAA GTG TAC ATC ATC      2544
Ala Ser Val Ala Leu Gly Met Leu Tyr Met Pro Lys Val Tyr Ile Ile
        835                 840                 845

ATT TTC CAC CCT GAA CTC AAT GTC CAG AAA CGG AAG CGA AGC TTC AAG      2592
Ile Phe His Pro Glu Leu Asn Val Gln Lys Arg Lys Arg Ser Phe Lys
    850                 855                 860
```

```
GCG GTA GTC ACA GCA GCC ACC ATG TCA TCG AGG CTG TCA CAC AAA CCC     2640
Ala Val Val Thr Ala Ala Thr Met Ser Ser Arg Leu Ser His Lys Pro
865                 870                 875                 880

AGT GAC AGA CCC AAC GGT GAG GCA AAG ACC GAG CTC TGT GAA AAC GTA     2688
Ser Asp Arg Pro Asn Gly Glu Ala Lys Thr Glu Leu Cys Glu Asn Val
                885                 890                 895

GAC CCA AAC AGC CCT GCT GCA AAA AAG AAG TAT GTC AGT TAT AAT AAC     2736
Asp Pro Asn Ser Pro Ala Ala Lys Lys Lys Tyr Val Ser Tyr Asn Asn
            900                 905                 910

CTG GTT ATC TA                                                     2748
Leu Val Ile
        915
```

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 915 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```
Met Val Gln Leu Arg Lys Leu Leu Arg Val Leu Thr Leu Met Lys Phe
 1               5                  10                  15

Pro Cys Cys Val Leu Glu Val Leu Leu Cys Ala Leu Ala Ala Ala Ala
            20                  25                  30

Arg Gly Gln Glu Met Tyr Ala Pro His Ser Ile Arg Ile Glu Gly Asp
        35                  40                  45
```

Val Thr Leu Gly Gly Leu Phe Pro Val His Ala Lys Gly Pro Ser Gly
50 55 60

Val Pro Cys Gly Asp Ile Lys Arg Glu Asn Gly Ile His Arg Leu Glu
65 70 75 80

Ala Met Leu Tyr Ala Leu Asp Gln Ile Asn Ser Asp Pro Asn Leu Leu
85 90 95

Pro Asn Val Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp
100 105 110

Thr Tyr Ala Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Gln
115 120 125

Lys Asp Thr Ser Asp Val Arg Cys Thr Asn Gly Glu Pro Pro Val Phe
130 135 140

Val Lys Pro Glu Lys Val Val Gly Val Ile Gly Ala Ser Gly Ser Ser
145 150 155 160

Val Ser Ile Met Val Ala Asn Ile Leu Arg Leu Phe Gln Ile Pro Gln
165 170 175

Ile Ser Tyr Ala Ser Thr Ala Pro Glu Leu Ser Asp Asp Arg Arg Tyr
180 185 190

Asp Phe Phe Ser Arg Val Val Pro Pro Asp Ser Phe Gln Ala Gln Ala
195 200 205

Met Val Asp Ile Val Lys Ala Leu Gly Trp Asn Tyr Val Ser Thr Leu
210 215 220

Ala Ser Glu Gly Ser Tyr Gly Glu Lys Gly Val Glu Ser Phe Thr Gln
225 230 235 240

Ile Ser Lys Glu Ala Gly Gly Leu Cys Ile Ala Gln Ser Val Arg Ile
245 250 255

Pro Gln Glu Arg Lys Asp Arg Thr Ile Asp Phe Asp Arg Ile Ile Lys
260 265 270

Gln Leu Leu Asp Thr Pro Asn Ser Arg Ala Val Val Ile Phe Ala Asn
275 280 285

Asp Glu Asp Ile Lys Gln Ile Leu Ala Ala Ala Lys Arg Ala Asp Gln
290 295 300

Val Gly His Phe Leu Trp Val Gly Ser Asp Ser Trp Gly Ser Lys Ile
305 310 315 320

Asn Pro Leu His Gln His Glu Asp Ile Ala Glu Gly Ala Ile Thr Ile
325 330 335

Gln Pro Lys Arg Ala Thr Val Glu Gly Phe Asp Ala Tyr Phe Thr Ser
340 345 350

Arg Thr Leu Glu Asn Asn Arg Arg Asn Val Trp Phe Ala Glu Tyr Trp
355 360 365

Glu Glu Asn Phe Asn Cys Lys Leu Thr Ile Ser Gly Ser Lys Lys Glu
370 375 380

Asp Thr Asp Arg Lys Cys Thr Gly Gln Glu Arg Ile Gly Lys Asp Ser
385 390 395 400

Asn Tyr Glu Gln Glu Gly Lys Val Gln Phe Val Ile Asp Ala Val Tyr
405 410 415

Ala Met Ala His Ala Leu His His Met Asn Lys Asp Leu Cys Ala Asp
420 425 430

Tyr Arg Gly Val Cys Pro Glu Met Glu Gln Ala Gly Gly Lys Lys Leu
435 440 445

Leu Lys Tyr Ile Arg Asn Val Asn Phe Asn Gly Ser Ala Gly Thr Pro
450 455 460

Val Met Phe Asn Lys Asn Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe
465 470 475 480

Gln Tyr Gln Thr Thr Asn Thr Ser Asn Pro Gly Tyr Arg Leu Ile Gly
485 490 495

Gln Trp Thr Asp Glu Leu Gln Leu Asn Ile Glu Asp Met Gln Trp Gly
500 505 510

Lys Gly Val Arg Glu Ile Pro Ala Ser Val Cys Thr Leu Pro Cys Lys
515 520 525

Pro Gly Gln Arg Lys Lys Thr Gln Lys Gly Thr Pro Cys Cys Trp Thr
530 535 540

Cys Glu Pro Cys Asp Gly Tyr Gln Tyr Gln Phe Asp Glu Met Thr Cys
545 550 555 560

Gln His Cys Pro Tyr Asp Gln Arg Pro Asn Glu Asn Arg Thr Gly Cys
565 570 575

Gln Asp Ile Pro Ile Ile Lys Leu Glu Trp His Ser Pro Trp Ala Val
580 585 590

Ile Pro Val Phe Leu Ala Met Leu Gly Ile Ile Ala Thr Ile Phe Val
595 600 605

Met Ala Thr Phe Ile Arg Tyr Asn Asp Thr Pro Ile Val Arg Ala Ser
610 615 620

```
Gly Arg Glu Leu Ser Tyr Val Leu Leu Thr Gly Ile Phe Leu Cys Tyr
625                 630                 635                 640

Ile Ile Thr Phe Leu Met Ile Ala Lys Pro Asp Val Ala Val Cys Ser
                645                 650                 655

Phe Arg Arg Val Phe Leu Gly Leu Gly Met Cys Ile Ser Tyr Ala Ala
            660                 665                 670

Leu Leu Thr Lys Thr Asn Arg Ile Tyr Arg Ile Phe Glu Gln Gly Lys
        675                 680                 685

Lys Ser Val Thr Ala Pro Arg Leu Ile Ser Pro Thr Ser Gln Leu Ala
    690                 695                 700

Ile Thr Ser Ser Leu Ile Ser Val Gln Leu Leu Gly Val Phe Ile Trp
705                 710                 715                 720

Phe Gly Val Asp Pro Pro Asn Ile Ile Ile Asp Tyr Asp Glu His Lys
                725                 730                 735

Thr Met Asn Pro Glu Gln Ala Arg Gly Val Leu Lys Cys Asp Ile Thr
            740                 745                 750

Asp Leu Gln Ile Ile Cys Ser Leu Gly Tyr Ser Ile Leu Leu Met Val
        755                 760                 765

Thr Cys Thr Val Tyr Ala Ile Lys Thr Arg Gly Val Pro Glu Asn Phe
    770                 775                 780

Asn Glu Ala Lys Pro Ile Gly Phe Thr Met Tyr Thr Thr Cys Ile Val
785                 790                 795                 800

Trp Leu Ala Phe Ile Pro Ile Phe Phe Gly Thr Ala Gln Ser Ala Glu
                805                 810                 815
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```
Lys Leu Tyr Ile Gln Thr Thr Thr Leu Thr Ile Ser Met Asn Leu Ser
            820                 825                 830

Ala Ser Val Ala Leu Gly Met Leu Tyr Met Pro Lys Val Tyr Ile Ile
        835                 840                 845

Ile Phe His Pro Glu Leu Asn Val Gln Lys Arg Lys Arg Ser Phe Lys
    850                 855                 860

Ala Val Val Thr Ala Ala Thr Met Ser Ser Arg Leu Ser His Lys Pro
865                 870                 875                 880

Ser Asp Arg Pro Asn Gly Glu Ala Lys Thr Glu Leu Cys Glu Asn Val
                885                 890                 895

Asp Pro Asn Ser Pro Ala Ala Lys Lys Lys Tyr Val Ser Tyr Asn Asn
            900                 905                 910

Leu Val Ile
        915
```

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2769 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS

(B) LOCATION: 1..2769

(D) OTHER INFORMATION: /product= "hmGluR7b"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```
ATG GTC CAG CTG AGG AAG CTG CTC CGC GTC CTG ACT TTG ATG AAG TTC      48
Met Val Gln Leu Arg Lys Leu Leu Arg Val Leu Thr Leu Met Lys Phe
 1               5                  10                  15

CCC TGC TGC GTG CTG GAG GTG CTC CTG TGC GCG CTG GCG GCG GCG GCG      96
Pro Cys Cys Val Leu Glu Val Leu Leu Cys Ala Leu Ala Ala Ala Ala
            20                  25                  30

CGC GGC CAG GAG ATG TAC GCC CCG CAC TCA ATC CGG ATC GAG GGG GAC     144
Arg Gly Gln Glu Met Tyr Ala Pro His Ser Ile Arg Ile Glu Gly Asp
        35                  40                  45

GTC ACC CTC GGG GGG CTG TTC CCC GTA CAC GCC AAG GGT CCC AGC GGA     192
Val Thr Leu Gly Gly Leu Phe Pro Val His Ala Lys Gly Pro Ser Gly
    50                  55                  60

GTG CCC TGC GGC GAC ATC AAG AGG GAA AAC GGG ATC CAC AGG CTG GAA     240
Val Pro Cys Gly Asp Ile Lys Arg Glu Asn Gly Ile His Arg Leu Glu
65                  70                  75                  80

GCG ATG CTC TAC GCC CTG GAC CAG ATC AAC AGT GAT CCC AAC CTA CTG     288
Ala Met Leu Tyr Ala Leu Asp Gln Ile Asn Ser Asp Pro Asn Leu Leu
                85                  90                  95

CCC AAC GTG ACG CTG GGC GCG CGG ATC CTG GAC ACT TGT TCC AGG GAC     336
Pro Asn Val Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp
            100                 105                 110
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ACT TAC GCG CTC GAA CAG TCG CTT ACT TTC GTC CAG GCG CTC ATC CAG      384
Thr Tyr Ala Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Gln
        115                 120                 125

AAG GAC ACC TCC GAC GTG CGC TGC ACC AAC GGC GAA CCG CCG GTT TTC      432
Lys Asp Thr Ser Asp Val Arg Cys Thr Asn Gly Glu Pro Pro Val Phe
    130                 135                 140

GTC AAG CCG GAG AAA GTA GTT GGA GTG ATT GGG GCT TCG GGG AGT TCG      480
Val Lys Pro Glu Lys Val Val Gly Val Ile Gly Ala Ser Gly Ser Ser
145                 150                 155                 160

GTC TCC ATC ATG GTA GCC AAC ATC CTG AGG CTC TTC CAG ATC CCC CAG      528
Val Ser Ile Met Val Ala Asn Ile Leu Arg Leu Phe Gln Ile Pro Gln
                165                 170                 175

ATT AGT TAT GCA TCA ACG GCA CCC GAG CTA AGT GAT GAC CGG CGC TAT      576
Ile Ser Tyr Ala Ser Thr Ala Pro Glu Leu Ser Asp Asp Arg Arg Tyr
            180                 185                 190

GAC TTC TTC TCT CGC GTG GTG CCA CCC GAT TCC TTC CAA GCC CAG GCC      624
Asp Phe Phe Ser Arg Val Val Pro Pro Asp Ser Phe Gln Ala Gln Ala
        195                 200                 205

ATG GTA GAC ATT GTA AAG GCC CTA GGC TGG AAT TAT GTG TCT ACC CTC      672
Met Val Asp Ile Val Lys Ala Leu Gly Trp Asn Tyr Val Ser Thr Leu
    210                 215                 220

GCA TCG GAA GGA AGT TAT GGA GAG AAA GGT GTG GAG TCC TTC ACG CAG      720
Ala Ser Glu Gly Ser Tyr Gly Glu Lys Gly Val Glu Ser Phe Thr Gln
225                 230                 235                 240

ATT TCC AAA GAG GCA GGT GGA CTC TGC ATT GCC CAG TCC GTG AGA ATC      768
Ile Ser Lys Glu Ala Gly Gly Leu Cys Ile Ala Gln Ser Val Arg Ile
                245                 250                 255
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CCC CAG GAA CGC AAA GAC AGG ACC ATT GAC TTT GAT AGA ATT ATC AAA      816
Pro Gln Glu Arg Lys Asp Arg Thr Ile Asp Phe Asp Arg Ile Ile Lys
            260                 265                 270

CAG CTC CTG GAC ACC CCC AAC TCC AGG GCC GTC GTG ATT TTT GCC AAC      864
Gln Leu Leu Asp Thr Pro Asn Ser Arg Ala Val Val Ile Phe Ala Asn
        275                 280                 285

GAT GAG GAT ATA AAG CAG ATC CTT GCA GCA GCC AAA AGA GCT GAC CAA      912
Asp Glu Asp Ile Lys Gln Ile Leu Ala Ala Ala Lys Arg Ala Asp Gln
    290                 295                 300

GTT GGC CAT TTT CTT TGG GTG GGA TCA GAC AGC TGG GGA TCC AAA ATA      960
Val Gly His Phe Leu Trp Val Gly Ser Asp Ser Trp Gly Ser Lys Ile
305                 310                 315                 320

AAC CCA CTG CAC CAG CAT GAA GAT ATC GCA GAA GGG GCC ATC ACC ATT     1008
Asn Pro Leu His Gln His Glu Asp Ile Ala Glu Gly Ala Ile Thr Ile
                325                 330                 335

CAG CCC AAG CGA GCC ACG GTG GAA GGG TTT GAT GCC TAC TTT ACG TCC     1056
Gln Pro Lys Arg Ala Thr Val Glu Gly Phe Asp Ala Tyr Phe Thr Ser
            340                 345                 350

CGT ACA CTT GAA AAC AAC AGA AGA AAT GTA TGG TTT GCC GAA TAC TGG     1104
Arg Thr Leu Glu Asn Asn Arg Arg Asn Val Trp Phe Ala Glu Tyr Trp
        355                 360                 365

GAG GAA AAC TTC AAC TGC AAG TTG ACG ATT AGT GGG TCA AAA AAA GAA     1152
Glu Glu Asn Phe Asn Cys Lys Leu Thr Ile Ser Gly Ser Lys Lys Glu
    370                 375                 380

GAC ACA GAT CGC AAA TGC ACA GGA CAG GAG AGA ATT GGA AAA GAT TCC     1200
Asp Thr Asp Arg Lys Cys Thr Gly Gln Glu Arg Ile Gly Lys Asp Ser
385                 390                 395                 400
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AAC TAT GAG CAG GAG GGT AAA GTC CAG TTC GTG ATT GAC GCA GTC TAT     1248
Asn Tyr Glu Gln Glu Gly Lys Val Gln Phe Val Ile Asp Ala Val Tyr
                405                 410                 415

GCT ATG GCT CAC GCC CTT CAC CAC ATG AAC AAG GAT CTC TGT GCT GAC     1296
Ala Met Ala His Ala Leu His His Met Asn Lys Asp Leu Cys Ala Asp
            420                 425                 430

TAC CGG GGT GTC TGC CCA GAG ATG GAG CAA GCT GGA GGC AAG AAG TTG     1344
Tyr Arg Gly Val Cys Pro Glu Met Glu Gln Ala Gly Gly Lys Lys Leu
        435                 440                 445

CTG AAG TAT ATA CGC AAT GTT AAT TTC AAT GGT AGT GCT GGC ACT CCA     1392
Leu Lys Tyr Ile Arg Asn Val Asn Phe Asn Gly Ser Ala Gly Thr Pro
    450                 455                 460

GTG ATG TTT AAC AAG AAC GGG GAT GCA CCT GGG CGT TAT GAC ATC TTT     1440
Val Met Phe Asn Lys Asn Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe
465                 470                 475                 480

CAG TAC CAG ACC ACA AAC ACC AGC AAC CCG GGT TAC CGT CTG ATC GGG     1488
Gln Tyr Gln Thr Thr Asn Thr Ser Asn Pro Gly Tyr Arg Leu Ile Gly
                485                 490                 495

CAG TGG ACA GAC GAA CTT CAG CTC AAT ATA GAA GAC ATG CAG TGG GGT     1536
Gln Trp Thr Asp Glu Leu Gln Leu Asn Ile Glu Asp Met Gln Trp Gly
            500                 505                 510

AAA GGA GTC CGA GAG ATA CCC GCC TCA GTG TGC ACA CTA CCA TGT AAG     1584
Lys Gly Val Arg Glu Ile Pro Ala Ser Val Cys Thr Leu Pro Cys Lys
        515                 520                 525

CCA GGA CAG AGA AAG AAG ACA CAG AAA GGA ACT CCT TGC TGT TGG ACC     1632
Pro Gly Gln Arg Lys Lys Thr Gln Lys Gly Thr Pro Cys Cys Trp Thr
    530                 535                 540
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TGT GAG CCT TGC GAT GGT TAC CAG TAC CAG TTT GAT GAG ATG ACA TGC     1680
Cys Glu Pro Cys Asp Gly Tyr Gln Tyr Gln Phe Asp Glu Met Thr Cys
545                 550                 555                 560

CAG CAT TGC CCC TAT GAC CAG AGG CCC AAT GAA AAT CGA ACC GGA TGC     1728
Gln His Cys Pro Tyr Asp Gln Arg Pro Asn Glu Asn Arg Thr Gly Cys
                565                 570                 575

CAG GAT ATT CCC ATC ATC AAA CTG GAG TGG CAC TCC CCC TGG GCT GTG     1776
Gln Asp Ile Pro Ile Ile Lys Leu Glu Trp His Ser Pro Trp Ala Val
            580                 585                 590

ATT CCT GTC TTC CTG GCA ATG TTG GGG ATC ATT GCC ACC ATC TTT GTC     1824
Ile Pro Val Phe Leu Ala Met Leu Gly Ile Ile Ala Thr Ile Phe Val
        595                 600                 605

ATG GCC ACT TTC ATC CGC TAC AAT GAC ACG CCC ATT GTC CGG GCA TCT     1872
Met Ala Thr Phe Ile Arg Tyr Asn Asp Thr Pro Ile Val Arg Ala Ser
    610                 615                 620

GGG CGG GAA CTC AGC TAT GTT CTT TTG ACG GGC ATC TTT CTT TGC TAC     1920
Gly Arg Glu Leu Ser Tyr Val Leu Leu Thr Gly Ile Phe Leu Cys Tyr
625                 630                 635                 640

ATC ATC ACT TTC CTG ATG ATT GCC AAA CCA GAT GTG GCA GTG TGT TCT     1968
Ile Ile Thr Phe Leu Met Ile Ala Lys Pro Asp Val Ala Val Cys Ser
                645                 650                 655

TTC CGG CGA GTT TTC TTG GGC TTG GGT ATG TGC ATC AGT TAT GCA GCC     2016
Phe Arg Arg Val Phe Leu Gly Leu Gly Met Cys Ile Ser Tyr Ala Ala
            660                 665                 670

CTC TTG ACG AAA ACA AAT CGG ATT TAT CGC ATA TTT GAG CAG GGC AAG     2064
Leu Leu Thr Lys Thr Asn Arg Ile Tyr Arg Ile Phe Glu Gln Gly Lys
        675                 680                 685
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AAA TCA GTA ACA GCT CCC AGA CTC ATA AGC CCA ACA TCA CAA CTG GCA      2112
Lys Ser Val Thr Ala Pro Arg Leu Ile Ser Pro Thr Ser Gln Leu Ala
    690                 695                 700

ATC ACT TCC AGT TTA ATA TCA GTT CAG CTT CTA GGG GTG TTC ATT TGG      2160
Ile Thr Ser Ser Leu Ile Ser Val Gln Leu Leu Gly Val Phe Ile Trp
705                 710                 715                 720

TTT GGT GTT GAT CCA CCC AAC ATC ATC ATA GAC TAC GAT GAA CAC AAG      2208
Phe Gly Val Asp Pro Pro Asn Ile Ile Ile Asp Tyr Asp Glu His Lys
                725                 730                 735

ACA ATG AAC CCT GAG CAA GCC AGA GGG GTT CTC AAG TGT GAC ATT ACA      2256
Thr Met Asn Pro Glu Gln Ala Arg Gly Val Leu Lys Cys Asp Ile Thr
            740                 745                 750

GAT CTC CAA ATC ATT TGC TCC TTG GGA TAT AGC ATT CTT CTC ATG GTC      2304
Asp Leu Gln Ile Ile Cys Ser Leu Gly Tyr Ser Ile Leu Leu Met Val
        755                 760                 765

ACA TGT ACT GTG TAT GCC ATC AAG ACT CGG GGT GTA CCC GAG AAT TTT      2352
Thr Cys Thr Val Tyr Ala Ile Lys Thr Arg Gly Val Pro Glu Asn Phe
    770                 775                 780

AAC GAA GCC AAG CCC ATT GGA TTC ACT ATG TAC ACG ACA TGT ATA GTA      2400
Asn Glu Ala Lys Pro Ile Gly Phe Thr Met Tyr Thr Thr Cys Ile Val
785                 790                 795                 800

TGG CTT GCC TTC ATT CCA ATT TTT TTT GGC ACC GCT CAA TCA GCG GAA      2448
Trp Leu Ala Phe Ile Pro Ile Phe Phe Gly Thr Ala Gln Ser Ala Glu
                805                 810                 815

AAG CTC TAC ATA CAA ACT ACC ACG CTT ACA ATC TCC ATG AAC CTA AGT      2496
Lys Leu Tyr Ile Gln Thr Thr Thr Leu Thr Ile Ser Met Asn Leu Ser
            820                 825                 830
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GCA TCA GTG GCG CTG GGG ATG CTA TAC ATG CCG AAA GTG TAC ATC ATC     2544
Ala Ser Val Ala Leu Gly Met Leu Tyr Met Pro Lys Val Tyr Ile Ile
        835                 840                 845

ATT TTC CAC CCT GAA CTC AAT GTC CAG AAA CGG AAG CGA AGC TTC AAG     2592
Ile Phe His Pro Glu Leu Asn Val Gln Lys Arg Lys Arg Ser Phe Lys
    850                 855                 860

GCG GTA GTC ACA GCA GCC ACC ATG TCA TCG AGG CTG TCA CAC AAA CCC     2640
Ala Val Val Thr Ala Ala Thr Met Ser Ser Arg Leu Ser His Lys Pro
865                 870                 875                 880

AGT GAC AGA CCC AAC GGT GAG GCA AAG ACC GAG CTC TGT GAA AAC GTA     2688
Ser Asp Arg Pro Asn Gly Glu Ala Lys Thr Glu Leu Cys Glu Asn Val
                885                 890                 895

GAC CCA AAC AAC TGT ATA CCA CCA GTA AGA AAG AGT GTA CAA AAG TCT     2736
Asp Pro Asn Asn Cys Ile Pro Pro Val Arg Lys Ser Val Gln Lys Ser
        900                 905                 910

GTT ACT TGG TAC ACT ATC CCA CCA ACA GTA TA                         2769
Val Thr Trp Tyr Thr Ile Pro Pro Thr Val
        915                 920
```

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 922 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```
Met Val Gln Leu Arg Lys Leu Leu Arg Val Leu Thr Leu Met Lys Phe
 1               5                  10                  15

Pro Cys Cys Val Leu Glu Val Leu Leu Cys Ala Leu Ala Ala Ala Ala
            20                  25                  30

Arg Gly Gln Glu Met Tyr Ala Pro His Ser Ile Arg Ile Glu Gly Asp
        35                  40                  45

Val Thr Leu Gly Gly Leu Phe Pro Val His Ala Lys Gly Pro Ser Gly
    50                  55                  60

Val Pro Cys Gly Asp Ile Lys Arg Glu Asn Gly Ile His Arg Leu Glu
65                  70                  75                  80

Ala Met Leu Tyr Ala Leu Asp Gln Ile Asn Ser Asp Pro Asn Leu Leu
                85                  90                  95

Pro Asn Val Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp
            100                 105                 110

Thr Tyr Ala Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Gln
        115                 120                 125

Lys Asp Thr Ser Asp Val Arg Cys Thr Asn Gly Glu Pro Pro Val Phe
    130                 135                 140

Val Lys Pro Glu Lys Val Val Gly Val Ile Gly Ala Ser Gly Ser Ser
145                 150                 155                 160

Val Ser Ile Met Val Ala Asn Ile Leu Arg Leu Phe Gln Ile Pro Gln
                165                 170                 175

Ile Ser Tyr Ala Ser Thr Ala Pro Glu Leu Ser Asp Asp Arg Arg Tyr
            180                 185                 190
```

Asp Phe Phe Ser Arg Val Val Pro Pro Asp Ser Phe Gln Ala Gln Ala
195 200 205

Met Val Asp Ile Val Lys Ala Leu Gly Trp Asn Tyr Val Ser Thr Leu
210 215 220

Ala Ser Glu Gly Ser Tyr Gly Glu Lys Gly Val Glu Ser Phe Thr Gln
225 230 235 240

Ile Ser Lys Glu Ala Gly Gly Leu Cys Ile Ala Gln Ser Val Arg Ile
245 250 255

Pro Gln Glu Arg Lys Asp Arg Thr Ile Asp Phe Asp Arg Ile Ile Lys
260 265 270

Gln Leu Leu Asp Thr Pro Asn Ser Arg Ala Val Val Ile Phe Ala Asn
275 280 285

Asp Glu Asp Ile Lys Gln Ile Leu Ala Ala Ala Lys Arg Ala Asp Gln
290 295 300

Val Gly His Phe Leu Trp Val Gly Ser Asp Ser Trp Gly Ser Lys Ile
305 310 315 320

Asn Pro Leu His Gln His Glu Asp Ile Ala Glu Gly Ala Ile Thr Ile
325 330 335

Gln Pro Lys Arg Ala Thr Val Glu Gly Phe Asp Ala Tyr Phe Thr Ser
340 345 350

Arg Thr Leu Glu Asn Asn Arg Arg Asn Val Trp Phe Ala Glu Tyr Trp
355 360 365

Glu Glu Asn Phe Asn Cys Lys Leu Thr Ile Ser Gly Ser Lys Lys Glu
370 375 380

```
Asp Thr Asp Arg Lys Cys Thr Gly Gln Glu Arg Ile Gly Lys Asp Ser
385                 390                 395                 400

Asn Tyr Glu Gln Glu Gly Lys Val Gln Phe Val Ile Asp Ala Val Tyr
                405                 410                 415

Ala Met Ala His Ala Leu His His Met Asn Lys Asp Leu Cys Ala Asp
            420                 425                 430

Tyr Arg Gly Val Cys Pro Glu Met Glu Gln Ala Gly Gly Lys Lys Leu
        435                 440                 445

Leu Lys Tyr Ile Arg Asn Val Asn Phe Asn Gly Ser Ala Gly Thr Pro
    450                 455                 460

Val Met Phe Asn Lys Asn Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe
465                 470                 475                 480

Gln Tyr Gln Thr Thr Asn Thr Ser Asn Pro Gly Tyr Arg Leu Ile Gly
                485                 490                 495

Gln Trp Thr Asp Glu Leu Gln Leu Asn Ile Glu Asp Met Gln Trp Gly
            500                 505                 510

Lys Gly Val Arg Glu Ile Pro Ala Ser Val Cys Thr Leu Pro Cys Lys
        515                 520                 525

Pro Gly Gln Arg Lys Lys Thr Gln Lys Gly Thr Pro Cys Cys Trp Thr
    530                 535                 540

Cys Glu Pro Cys Asp Gly Tyr Gln Tyr Gln Phe Asp Glu Met Thr Cys
545                 550                 555                 560

Gln His Cys Pro Tyr Asp Gln Arg Pro Asn Glu Asn Arg Thr Gly Cys
                565                 570                 575
```

Gln Asp Ile Pro Ile Ile Lys Leu Glu Trp His Ser Pro Trp Ala Val
580 585 590

Ile Pro Val Phe Leu Ala Met Leu Gly Ile Ile Ala Thr Ile Phe Val
595 600 605

Met Ala Thr Phe Ile Arg Tyr Asn Asp Thr Pro Ile Val Arg Ala Ser
610 615 620

Gly Arg Glu Leu Ser Tyr Val Leu Leu Thr Gly Ile Phe Leu Cys Tyr
625 630 635 640

Ile Ile Thr Phe Leu Met Ile Ala Lys Pro Asp Val Ala Val Cys Ser
645 650 655

Phe Arg Arg Val Phe Leu Gly Leu Gly Met Cys Ile Ser Tyr Ala Ala
660 665 670

Leu Leu Thr Lys Thr Asn Arg Ile Tyr Arg Ile Phe Glu Gln Gly Lys
675 680 685

Lys Ser Val Thr Ala Pro Arg Leu Ile Ser Pro Thr Ser Gln Leu Ala
690 695 700

Ile Thr Ser Ser Leu Ile Ser Val Gln Leu Leu Gly Val Phe Ile Trp
705 710 715 720

Phe Gly Val Asp Pro Pro Asn Ile Ile Ile Asp Tyr Asp Glu His Lys
725 730 735

Thr Met Asn Pro Glu Gln Ala Arg Gly Val Leu Lys Cys Asp Ile Thr
740 745 750

Asp Leu Gln Ile Ile Cys Ser Leu Gly Tyr Ser Ile Leu Leu Met Val
755 760 765

Thr Cys Thr Val Tyr Ala Ile Lys Thr Arg Gly Val Pro Glu Asn Phe
770 775 780

Asn Glu Ala Lys Pro Ile Gly Phe Thr Met Tyr Thr Thr Cys Ile Val
785 790 795 800

Trp Leu Ala Phe Ile Pro Ile Phe Phe Gly Thr Ala Gln Ser Ala Glu
805 810 815

Lys Leu Tyr Ile Gln Thr Thr Thr Leu Thr Ile Ser Met Asn Leu Ser
820 825 830

Ala Ser Val Ala Leu Gly Met Leu Tyr Met Pro Lys Val Tyr Ile Ile
835 840 845

Ile Phe His Pro Glu Leu Asn Val Gln Lys Arg Lys Arg Ser Phe Lys
850 855 860

Ala Val Val Thr Ala Ala Thr Met Ser Ser Arg Leu Ser His Lys Pro
865 870 875 880

Ser Asp Arg Pro Asn Gly Glu Ala Lys Thr Glu Leu Cys Glu Asn Val
885 890 895

Asp Pro Asn Asn Cys Ile Pro Pro Val Arg Lys Ser Val Gln Lys Ser
900 905 910

Val Thr Trp Tyr Thr Ile Pro Pro Thr Val
915 920

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 630 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..630
(D) OTHER INFORMATION: /product= "partial hmGluR6"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```
GTG GAG GCC CTG CAG TGG TCT GGC GAC CCC CAC GAG GTG CCC TCG TCT      48
Val Glu Ala Leu Gln Trp Ser Gly Asp Pro His Glu Val Pro Ser Ser
 1               5                  10                  15

CTG TGC AGC CTG CCC TGC GGG CCG GGG GAG CGG AAG AAG ATG GTG AAG      96
Leu Cys Ser Leu Pro Cys Gly Pro Gly Glu Arg Lys Lys Met Val Lys
            20                  25                  30

GGC GTC CCC TGC TGT TGG CAC TGC GAG GCC TGT GAC GGG TAC CGC TTC     144
Gly Val Pro Cys Cys Trp His Cys Glu Ala Cys Asp Gly Tyr Arg Phe
        35                  40                  45

CAG GTG GAC GAG TTC ACA TGC GAG GCC TGT CCT GGG TAC ATG AGG CCC     192
Gln Val Asp Glu Phe Thr Cys Glu Ala Cys Pro Gly Tyr Met Arg Pro
    50                  55                  60

ACN CCC AAC CAC ATC NNA CTT NNG CCC ACA CCT GTG GTG CGC CTG AGC     240
Xaa Pro Asn His Ile Xaa Leu Xaa Pro Thr Pro Val Val Arg Leu Ser
65                  70                  75                  80
```

```
TGG TCC TCC CCC TGG GCA GCC CCG CCG CTC CTC CTG GCC GTG CTG GGC      288
Trp Ser Ser Pro Trp Ala Ala Pro Pro Leu Leu Leu Ala Val Leu Gly
                    85                  90                  95

ATC GTG GCC ACT ACC ACG GTG GTG GCC ACC TTC GTG CGG TAC AAC AAC      336
Ile Val Ala Thr Thr Thr Val Val Ala Thr Phe Val Arg Tyr Asn Asn
            100                 105                 110

ACG CCC ATC GTC CGG GCC TCG GGC CGA GAG CTC AGC TAC GTC CTC CTC      384
Thr Pro Ile Val Arg Ala Ser Gly Arg Glu Leu Ser Tyr Val Leu Leu
        115                 120                 125

ACC GGC ATC TTC CTC ATC TAC GCC ATC ACC TTC CTC ATG GTG GCT GAG      432
Thr Gly Ile Phe Leu Ile Tyr Ala Ile Thr Phe Leu Met Val Ala Glu
    130                 135                 140

CCT GGG GCA GCG GTC TGT GCC GCC CGC AGG CTC TTC CTG GGC CTG GGC      480
Pro Gly Ala Ala Val Cys Ala Ala Arg Arg Leu Phe Leu Gly Leu Gly
145                 150                 155                 160

ACG ACC CTC AGC TAC TCT GCC CTG CTC ACC AAG ACC AAC CGT ATC TAC      528
Thr Thr Leu Ser Tyr Ser Ala Leu Leu Thr Lys Thr Asn Arg Ile Tyr
                165                 170                 175

CGC ATC TTT GAG CAG GGC AAG CGC TCG GTC ACA CCC CCT CCC TTC ATC      576
Arg Ile Phe Glu Gln Gly Lys Arg Ser Val Thr Pro Pro Pro Phe Ile
            180                 185                 190

AGC CCC ACC TCA CAG CTG GTC ATC ACC TTC AGC CTC ACC TCC CTG CAG      624
Ser Pro Thr Ser Gln Leu Val Ile Thr Phe Ser Leu Thr Ser Leu Gln
        195                 200                 205

GTG GGG                                                              630
Val Gly
    210
```

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```
Val Glu Ala Leu Gln Trp Ser Gly Asp Pro His Glu Val Pro Ser Ser
 1               5                  10                  15

Leu Cys Ser Leu Pro Cys Gly Pro Gly Glu Arg Lys Lys Met Val Lys
            20                  25                  30

Gly Val Pro Cys Cys Trp His Cys Glu Ala Cys Asp Gly Tyr Arg Phe
        35                  40                  45

Gln Val Asp Glu Phe Thr Cys Glu Ala Cys Pro Gly Tyr Met Arg Pro
    50                  55                  60

Xaa Pro Asn His Ile Xaa Leu Xaa Pro Thr Pro Val Val Arg Leu Ser
65                  70                  75                  80

Trp Ser Ser Pro Trp Ala Ala Pro Pro Leu Leu Leu Ala Val Leu Gly
                85                  90                  95

Ile Val Ala Thr Thr Thr Val Val Ala Thr Phe Val Arg Tyr Asn Asn
            100                 105                 110

Thr Pro Ile Val Arg Ala Ser Gly Arg Glu Leu Ser Tyr Val Leu Leu
        115                 120                 125
```

Thr Gly Ile Phe Leu Ile Tyr Ala Ile Thr Phe Leu Met Val Ala Glu
130 135 140

Pro Gly Ala Ala Val Cys Ala Ala Arg Arg Leu Phe Leu Gly Leu Gly
145 150 155 160

Thr Thr Leu Ser Tyr Ser Ala Leu Leu Thr Lys Thr Asn Arg Ile Tyr
165 170 175

Arg Ile Phe Glu Gln Gly Lys Arg Ser Val Thr Pro Pro Pro Phe Ile
180 185 190

Ser Pro Thr Ser Gln Leu Val Ile Thr Phe Ser Leu Thr Ser Leu Gln
195 200 205

Val Gly
210

Claims

1. Purified human metabotropic glutamate receptor (hmGluR) which is a member of the hmGluR4 subfamily.

2. A receptor of the hmGluR4 subfamily according to claim 1 characterized in that its amino acid sequence is more than about 65 % identical, particularly about 70 % identical, to the sequence of hmGluR4 set forth in SEQ ID NO:2.

3. Receptor according to claim 1 selected from the group consisting of hmGluR4, hmGluR7 and hmGluR6.

4. Receptor according to claim 2 which is a hmGluR4 subtype.

5. Receptor according to claim 2 which is the hmGluR4 subtype having the amino acid sequence set forth in SEQ ID NO:2.

6. Receptor according to claim 2 which is a hmGluR7 subtype.

7. Receptor according to claim 2 which is a hmGluR7 subtype selected from the group consisting of hmGluR7a having the amino acid sequence set forth in SEQ ID NO:12 and hmGluR7b having the amino acid sequence set forth in SEQ ID NO:14.

8. Receptor according to claim 2 which is a hmGluR7 subtype comprising a polypeptide selected from the group consisting of the polypeptides having the amino acid sequences set forth in SEQ ID NOs. 6, 8 and 10, respectively.

9. Receptor according to claim 2 which is a hmGluR6 subtype.

10. Receptor according to claim 2 which is a hmGluR6 subtype comprising a polypeptide having the amino acid sequence set forth in SEQ ID NO:16.

11. Variant of a receptor according to any of claims 1 to 10.

12. Composition of matter comprising a receptor of any of claims 1 to 11.

13. Process for the preparation of a receptor of any of claims 1 to 11 comprising multiplication of a suitable host cell in vitro or in vivo.

14. Use of a receptor according to any of claims 1 to 11 for screening of a compound which modulates the activity of said receptor.

15. Nucleic acid comprising a nucleic acid coding for a receptor according to any of claims 1 to claim 11, or a fragment of said nucleic acid.

16. Nucleic acid according to claim 15, which is a DNA.

17. A DNA according to claim 16 selected from the group consisting of the DNAs having substantially the nucleotide sequences set forth in SEQ ID Nos. 1, 3, 5, 7, 9, 11, 13 and 15, respectively.

18. Nucleic acid probe comprising at least 14 contiguous bases of the DNA according to claim 16 or 17, or the complement thereof.

19. Process for the preparation of a nucleic acid according to claim 16.

20. A DNA according to claim 17 which is a hybrid vector.

21. A host cell comprising a DNA of claim 17.

22. A eukaryotic host cell expressing the DNA of claim 17.

23. A host cell transfected with a DNA of claim 20.

24. A host cell according to claim 23 which is a mammalian cell.

25. Use of a host cell according to claim 22 for the screening of a compound which modulates the activity of a receptor according to claim 1.

26. Process for the preparation of a host cell according to claim 21.

27. Purified mRNA complementary to the DNA according to claim 7.

28. A method for identifying DNA encoding a hmGluR subtype according to claim 1 comprising: contacting human DNA with a probe according to claim 18, and identifying DNA(s) which substantially hybridize to said probe.

29. A method for identifying compounds binding to a hmGluR subtype comprising use of a receptor protein according to claim 1 in a competitive binding assay.

30. An assay for identifying compounds whcih modulate the activity of a hmGluR subtype according to claim 1 comprising
- contacting the cells of claim 22 with at least one compound or signal whose ability to modulate the activity of said receptor subtype is sought to be determined, and subsequently
- analyzing cells for a difference in functional response attributable to said receptor.

31. Assay according to claim 30 comprising
- contacting the cells of claim 22 with at least one compound or signal whose ability to modulate the second messenger activity of a receptor subtype of the invention is sought to be determined, and subsequently
- monitoring said cells for a change in the level of a particular second messenger.

32. A method for modulating the signal transduction activity of a hmGluR subtype according to claim 1 comprising contacting said subtype with an effective amount of at least one compound identified in the assay of claim 31.

33. An agonist, antagonist or allosteric modulator identified by the assay of claim 30.

34. A modulator of a hmGluR subtype according to claim 1 identified by the assay of claim 30.

35. A method for detecting a glutamate agonist or an allosteric modulator of a hmGluR subtype according to claim 1 having agonistic activity comprising the steps of (a) exposing a compound to a hmGluR subtype of the invention coupled to a response pathway, under conditions and for a time sufficient to allow interaction of the compound with the receptor and an associated response through the pathway, and (b) detecting an

increase or decrease in the stimulation of the response pathway resulting from the interaction of the compound with the hmGluR subtype, relative to the absence of the tested compound and therefrom determining the presence of an agonist or an allosteric modulator having agonist-like activity.

36. A method for identifying a glutamate antagonist or an allosteric modulator of a hmGluR subtype according to claim 1 having antagonistic activity, said method comprising the steps of (a) exposing a compound in the presence of a known glutamate agonist to a hmGluR subtype of the invention coupled to a response pathway, under conditions and for a time sufficient to allow interaction of the agonist with the receptor and an associated response through the pathway, and (b) detecting an inhibition of the stimulation of the response pathway by the agonist resulting from the interaction of the test compound with the hmGluR subtype, relative to the stimulation of the response pathway induced by the glutamate agonist alone, and therefrom determining the presence of a glutamate antagonist or an allosteric modulator having antagonist-like activity.

37. An antibody directed against a protein of claim 1.

38. An antibody according to claim 37 which is a polyclonal antibody.

39. An antibody according to claim 37 which is a monoclonal antibody.

40. A method for modulating the signal transduction activity of a hmGluR subtype according to claim 1 comprising contacting said receptor with an antibody of claim 35.

41. A receptor according to claim 1 obtainable by recombinant DNA technology.

42. A fusion protein comprising a receptor according to any of claims 1 to 11.

INTERNATIONAL SEARCH REPORT

Intern al Application No
PCT/EP 94/02991

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/12 C12N15/62 C07K14/705 C07K16/28 C12N5/10
C12Q1/68 G01N33/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N C07K C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	JOURNAL OF BIOLOGICAL CHEMISTRY., vol.269, no.2, 14 January 1994, BALTIMORE US pages 1231 - 1236 OKAMOTO N., HORI S., AKAZAWA C., HAYASHI Y., SHIGEMOTO R.,MIZUNO N., NAKANISHI S.; 'Molecular characterization of a new metabotropic glutamate receptor mGluR7 couple to inhibitory cyclic AMP signal transduction' see the whole document --- -/--	1,3,6-8, 11-28, 37-41

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

* Special categories of cited documents :

'A' document defining the general state of the art which is not considered to be of particular relevance

'E' earlier document but published on or after the international filing date

'L' document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

'O' document referring to an oral disclosure, use, exhibition or other means

'P' document published prior to the international filing date but later than the priority date claimed

'T' later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

'X' document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

'Y' document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

'&' document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
1 December 1994	14. 12. 94
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax (+31-70) 340-3016	Authorized officer Nauche, S

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INTERNATIONAL SEARCH REPORT

Inter. nal Application No
PCT/EP 94/02991

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	JOURNAL OF BIOLOGICAL CHEMISTRY., vol.268, no.16, 5 June 1993, BALTIMORE US pages 11868 - 11873 NAKAJIMA, Y. ET AL.; 'Molecular characterization of a novel retinal metabotropic glutamate receptor mGluR6 with a hgh agonist selectivitiy for L-2-Amino-4-phosphonobutyrate'	1-3, 9-26, 37-41
Y	see the whole document	29-36
X	NEURON, vol.8, 1992 pages 169 - 179 TANABE, Y. ET AL.; 'A family of metabotropic glutamate receptors'	1-5, 11-26, 37-41
Y	see the whole document	29-36
Y	WO,A,92 10583 (ZYMOGENETICS, INC, US) 25 June 1992 see page 19, line 1 - page 24, line 17; claims 31-38	29-36
A	WO,A,91 06648 (THE SALK INSTITUTE FOR BIOLOGICAL STUDIES, US) 16 May 1991	

1

INTERNATIONAL SEARCH REPORT

Information on patent family members

Inter. nal Application No
PCT/EP 94/02991

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
WO-A-9210583	25-06-92	AU-A-	9135691	08-07-92
		CA-A-	2098295	13-06-92
		EP-A-	0577605	12-01-94
		JP-T-	6503961	12-05-94
		NZ-A-	240921	27-06-94
WO-A-9106648	16-05-91	AU-B-	652349	25-08-94
		AU-A-	6639890	31-05-91
		EP-A-	0497884	12-08-92
		JP-T-	5508306	25-11-93
		US-A-	5202257	13-04-93